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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:09:54 ; Search time 225.955 Seconds
(without alignments)
349.180 Million cell updates/sec

Title: US-10-828-343-2

Perfect score: 1095

Sequence: 1 MCWFKLWSLLVGSLLVSGT.....GQAVRVLDSPDVPDVHDK 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	2 AAW40103	Aaw40103 Human her
2	1095	100.0	204	2 AAW23944	Aaw23944 Human her
3	1095	100.0	204	2 AAW74570	Aaw74570 Kaposi sa
4	992	90.6	185	2 AAW95015	Aaw95015 Kaposi's
5	188	17.2	184	2 AAW02611	Aaw02611 Interleuk
6	187	17.1	184	2 AAW02610	Aaw02610 Interleuk
7	186	17.0	183	8 ADL89593	Aaw08477 Interleuk
8	185.5	16.9	184	2 AAW08477	Aaw08477 Interleuk
9	185.5	16.9	570	6 ABP72702	Abp72702 Human int
10	184.5	16.8	184	2 AAW08476	Aaw08476 Interleuk
11	184	16.8	183	8 ADL89567	Adl89567 Human mod
12	184	16.8	201	1 AAP81162	Aap81162 Polypepti
13	184	16.8	212	5 AAU99248	Aau99248 Human int
14	184	16.8	212	5 AAU99249	Aau99249 Human int
15	184	16.8	212	5 AAU99250	Aau99250 Human int
16	184	16.8	212	5 AAU99601	Aau99601 Human int
17	183.5	16.8	184	2 AAW07200	Aaw07200 Human int
18	183.5	16.8	184	2 AAW58519	Aaw58519 Human int
19	183.5	16.8	184	2 AAW32803	Aaw32803 Human IL-
20	183.5	16.8	500	2 AAW36847	Aaw36847 Human fus
21	183.5	16.8	525	2 AAW36846	Aaw36846 Human fus
22	183	16.7	183	2 AAW77387	Aar77387 Human IL-
23	183	16.7	183	8 ADL89594	Adl89594 Human mod
24	183	16.7	183	8 ADL89586	Adl89586 Human mod
25	183	16.7	183	8 ADL89584	Adl89584 Human mod

26	183	16.7	183	8 ADL89566	Adl89566 Human mod
27	183	16.7	185	2 AAR45718	Aar45718 Full leng
28	183	16.7	185	2 AAR45720	Aar45720 Full leng
29	183	16.7	211	2 AAR25279	Aar25279 Mutant hu
30	183	16.7	212	1 AAP70238	Aap70238 Interfero
31	183	16.7	212	1 AAP80269	Aap80269 Recombina
32	183	16.7	212	1 AAP90469	Aap90469 Interleuk
33	183	16.7	212	1 AAP90436	Aap90436 Interfero
34	183	16.7	212	1 AAP90047	Aap90047 pBSF2-L8
35	183	16.7	212	1 AAP90371	Aap90371 pBSF2-L8
36	183	16.7	212	2 AAR05415	Aar05415 Human B-c
37	183	16.7	212	2 AAR33430	Aar33430 IFN-beta-
38	183	16.7	212	2 AAR34726	Aar34726 Human IL-
39	183	16.7	212	2 AAR49249	Aar49249 Sequence
40	183	16.7	212	2 AAR49041	Aar49041 Human int
41	183	16.7	212	2 AAR72317	Aar72317 Interfero
42	183	16.7	212	2 AAW33643	Aaw33643 Human int
43	183	16.7	212	2 AAW35878	Aaw35878 Human int
44	183	16.7	212	3 AAY87816	Aay87816 Human IL-
45	183	16.7	212	5 AAE15825	Aae15825 Human int

ALIGNMENTS

RESULT 1
AAW40103
ID AAW40103 standard; protein; 204 AA.

XX AAW40103;

XX

DT 27-AUG-2003 (revised)

DT 15-JUL-1998 (first entry)

XX

DE Human herpesvirus 8 (HHV-8) interleukin-6.

XX

KW DL-B; thymidylate synthase; dihydrofolate reductase; primer; HHV-8;

KW Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;

KW Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; VIL-6.

XX

OS Human herpesvirus 8.

XX

PN W09804284-A1.

XX

PD 05-FEB-1998.

XX

PF 24-JUL-1997; 97WO-US012931.

XX

PR 25-JUL-1996; 96US-0022591P.

XX

PA (UYJO) UNIV JOHNS HOPKINS.

XX

PI Hayward GS, Nicholas J, Reitz MR, Hardwick JM;

XX

WPI; 1998-130422/12.

DR

PT New human herpes virus gene region containing 8 open reading frames -
useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based large
cell lymphoma.

PT

PS Claim 1; Page 59-60; 84pp; English.

XX

CC The sequence represents a novel human herpesvirus 8 (HHV-8) interleukin-
6. The invention claims for novel genes, which includes the viral
interleukin-6 gene, found at the divergent DL-B locus. HHV-8 divergent
locus DL-B lies between open reading frames 11 and 17. Sequencing of the
HHV-8 divergent locus DL-B revealed the presence of nine viral ORFs with
gene products related to cellular proteins. These proteins include the
thymidylate synthase (TS, AAW40100), dihydrofolate reductase (DHFR, see
AAW40101), Bcl-2 homologue (AAW40102), IE-1A (AAW40107), IE-1B (AAW40108)
and, four cytokines which include viral interleukin-6 (VIL-6), viral
macrophage inhibitory protein (VMIP)-1A (AAW40104) and -1B (AAW40105) and
beta-chemokine-like (BCK, AAW40106) protein. The invention claims the

CC

CC mentioned proteins and a polynucleotide containing HHV-8 genes encoding
CC one or more of these proteins. The invention also claims that the
CC polynucleotide and the proteins may be used directly or indirectly, e.g.
CC using antibodies to the proteins, to diagnose an HHV-8 associated
CC disease, e.g. Kaposi's sarcoma, Castelman's disease, multiple myeloma and
CC body cavity based large cell lymphoma (BCBL). The proteins have also been
CC claimed to be useful in screening compounds for drugs to treat HHV-8
CC diseases. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ

Sequence 204 AA;
Query Match 100.0%; Score 1095; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.2e-117;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCWFKLSLLVSGSLVSGTRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCVRTGIC 60
DB 1 MCWFKLSLLVSGSLVSGTRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCVRTGIC 60
QY 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLKFLTTFEGKSVI 120
DB 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLKFLTTFEGKSVI 120
QY 121 NVDVMELLTKTLGWDIQBELNKLTKTHYSPKFDRLGLRQLGLKYWRHFASFVYLSAM 180
DB 121 NVDVMELLTKTLGWDIQBELNKLTKTHYSPKFDRLGLRQLGLKYWRHFASFVYLSAM 180
QY 181 EKFAQAVRVLDSPDVTDPVHDK 204
DB 181 EKFAQAVRVLDSPDVTDPVHDK 204

RESULT 2
AAW23944
ID AAW23944 standard; protein; 204 AA.
AC AAW23944;
XX
XX 30-JUN-1998 (first entry)
DE Human herpesvirus 8 interleukin-6.
KW interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
KW antibody; diagnosis; treatment.
XX
OS Human herpesvirus 8.
XX WO9803657-A1.
PN
XX 29-JAN-1998.
PD
XX 19-JUL-1996; 96WO-EP003199.
PF
XX 19-JUL-1996; 96WO-EP003199.
PR
XX (BEHW) BEHRING DIAGNOSTICS GMBH.
PA (UINY) UNIV NEW YORK STATE.
XX
PI Fleckenstein B, Albrecht J, Neipel F, Friedman-Kien A, Huang Y;
XX WPI; 1998-120781/11.
DR
XX

XX Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA
PT - and related nucleic acid and antibodies, used for diagnosis and
PT treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
XX
XX Claim 2; Fig 2; 19pp; English.
PS
XX The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence
CC can be used to detect antibodies and antibodies can be used to detect IL-
CC 6. This can be used for the diagnosis of HHV8 infection or associated
CC diseases such as Kaposi sarcoma or kidney cell carcinoma. Antibodies,
CC proteins and the gene sequence can all be used in the treatment of

CC infections and diseases as mentioned above
XX
SQ Sequence 204 AA;
Query Match 100.0%; Score 1095; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.2e-117;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCWFKLSLLVSGSLVSGTRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCVRTGIC 60
DB 1 MCWFKLSLLVSGSLVSGTRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCVRTGIC 60
QY 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLKFLTTFEGKSVI 120
DB 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKADGFEFEVLKFLTTFEGKSVI 120
QY 121 NVDVMELLTKTLGWDIQBELNKLTKTHYSPKFDRLGLRQLGLKYWRHFASFVYLSAM 180
DB 121 NVDVMELLTKTLGWDIQBELNKLTKTHYSPKFDRLGLRQLGLKYWRHFASFVYLSAM 180
QY 181 EKFAQAVRVLDSPDVTDPVHDK 204
DB 181 EKFAQAVRVLDSPDVTDPVHDK 204

RESULT 3
AAW74570
ID AAW74570 standard; protein; 204 AA.
XX
AC AAW74570;
XX
XX 04-DEC-1998 (first entry)
DT Kaposi sarcoma herpes-like virus/interleukin-6.
DE
XX Kaposi sarcoma herpes-like virus/interleukin-6; PCR; primer;
KW antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis;
KW monoclonal gammopathy of undetermined significance; MGUS; malignant;
KW interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma;
KW systemic lupus erythematosus; amplification.
XX
OS Synthetic.
XX
XX WO9835684-A2.
PN
XX 20-AUG-1998.
PD
XX 12-FEB-1998; 98WO-US002820.
PF
XX 14-FEB-1997; 97US-00800710.
PR
XX 11-NOV-1997; 97US-00967504.
PR
XX (BERE/) BERENSON J R.
PA (RETT/) RETTIG M B.
PA (VESC/) VESCIO R A.
XX
XX Berenson JR, Rettig MB, Vescio RA;
PI
XX WPI; 1998-480765/41.
DR
XX N-PSDB; AAV54070.
DR
XX Treatment of multiple myeloma and monoclonal myopathy with antiviral
PT agent - active against Kaposi sarcoma virus, or with inhibitory nucleic
PT acid or antibody against this virus.
XX
XX Disclosure; Fig 5B; 137pp; English.
PS
XX This is the amino acid sequence of the kaposi sarcoma herpes-like
CC virus/interleukin-6, used in the method of the invention. In this method,
CC an antiviral agent effective against Kaposi sarcoma herpes-like virus
CC (KSHV), is used to prevent progression of MGUS to multiple myeloma or
CC related malignancy. KHSV- and/or interleukin-6 related disorders such as
CC specifically Alzheimer's disease, multiple sclerosis, rheumatoid

CC arthritis, systemic lupus erythematosus, scleroderma and malignancies of
 CC kidney or head/neck. The vaccines (comprising a KHSV-specific immunogen)
 CC is used to produce a therapeutic and/or prophylactic response
 XX
 SQ Sequence 204 AA;
 Query Match 100.0%; Score 1095; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.2e-117;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MCFKLSLLVSGSLVSGTRGKLPDAPEEKLLIQLRNWMLWIDECFRDLCTRTGIC 60
 Db 1 MCFKLSLLVSGSLVSGTRGKLPDAPEEKLLIQLRNWMLWIDECFRDLCTRTGIC 60
 Qy 61 KGILEPAAIFHLKLPAINDDHCGLIGFNETSCLKKLADGFFFEVLFKELTFEFGKSVI 120
 Db 61 KGILEPAAIFHLKLPAINDDHCGLIGFNETSCLKKLADGFFFEVLFKELTFEFGKSVI 120
 Qy 121 NVDWELLTKLWIDIEELNKLTKTHYSPPKFDRGLLQGLKYWRHFFASFYVLSAM 180
 Db 121 NVDWELLTKLWIDIEELNKLTKTHYSPPKFDRGLLQGLKYWRHFFASFYVLSAM 180
 Qy 181 EKFAQAVRVLDSIPDVTVDHDK 204
 Db 181 EKFAQAVRVLDSIPDVTVDHDK 204

RESULT 4
 AAW95015
 ID AAW95015 standard; peptide; 185 AA.
 AC AAW95015;
 XX
 XX 27-AUG-2003 (revised)
 DT 21-MAY-1999 (first entry)
 XX
 XX Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.
 BE Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
 KW inflammatory condition; drug screening; human; IL-6.
 KW
 XX Human herpesvirus 8.
 OS
 XX WO9905280-A1.
 PN
 XX
 XX 04-FEB-1999.
 PD
 XX 24-JUL-1998; 98WO-US015423.
 PF
 XX 25-JUL-1997; 97US-00900905.
 PR
 XX (SCHE) SCHERING CORP.
 PA
 XX Bazan JF;
 PI
 XX WPI; 1999-142935/12.
 DR
 XX Newly isolated or recombinant polynucleotide encoding mammalian cytokine
 PT interleukin-B30 (IL-B30), including fragments - useful for regulating
 PT activation, development, differentiation and function of various cell
 PT types, and for diagnosing and treating conditions associated with IL-B30.
 XX
 XX Disclosure; Page 11-12; 83pp; English.
 PS
 XX This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
 CC polypeptides. Host cells containing a vector comprising the IL-B30
 CC nucleic acids are used for the recombinant production of the proteins.
 CC The polynucleotides are useful for diagnosis of IL-B30 mediated
 CC conditions, and forensic science (e.g. to distinguish rodent from human,
 CC or as a marker to distinguish between different cells exhibiting
 CC differential expression or modification patterns). The IL-B30 (including
 CC fragments), together with antibodies that bind to IL-B30 are useful for
 CC teaching purposes. They are also used for treating conditions associated

CC with abnormal physiology or development, including inflammatory
 CC conditions. The polypeptide cytokine should mediate cytokine synthesis
 CC and proliferation in cells. IL-B30 is useful for drug screening to
 CC identify compounds having binding affinity to IL-B30. The present
 CC -AUG-2003 to correct OS field.)
 XX
 SQ Sequence 185 AA;
 Query Match 90.6%; Score 992; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 8.2e-106;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 20 TRGKLPDAPEFEKLLIQLRNWMLWIDECFRDLCTRTGICGKILEPAAIFHLKLPAIND 79
 Db 1 TRGKLPDAPEFEKLLIQLRNWMLWIDECFRDLCTRTGICGKILEPAAIFHLKLPAIND 60
 Qy 80 TDHCGLIGFNETSCLKKLADGFFFEVLFKELTFEFGKSVINVDWELLTKLWIDIEOE 139
 Db 61 TDHCGLIGFNETSCLKKLADGFFFEVLFKELTFEFGKSVINVDWELLTKLWIDIEOE 120
 Qy 140 LNKLTTHYSPPKFDRGLLQGLKYWRHFFASFYVLSAMEKFAQAVRVLDSIPDVTTP 199
 Db 121 LNKLTTHYSPPKFDRGLLQGLKYWRHFFASFYVLSAMEKFAQAVRVLDSIPDVTTP 180
 Qy 200 DVHDK 204
 Db 181 DVHDK 185
 RESULT 5
 AAW02611
 ID AAW02611 standard; protein; 184 AA.
 AC AAW02611;
 XX
 XX 25-MAR-2003 (revised)
 DT 24-FEB-1997 (first entry)
 XX
 DE Interleukin-6 (F74Y, Q75P, S76I, Q175I, S176R, Q183A).
 XX
 KW Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
 KW bovine; granulocyte colony stimulating factor; bc-CSF; receptor; gp130;
 KW thrombocytopoiesis; haematopoietic progenitor cell; rheumatoid arthritis;
 KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
 KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
 KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
 OS
 XX Homo sapiens.
 PH
 FT Key Location/Qualifiers
 FT Misc-difference 74 /note= "F74Y"
 FT Misc-difference 75 /note= "Q75P"
 FT Misc-difference 76 /note= "S76I"
 FT Misc-difference 175 /note= "Q175I"
 FT Misc-difference 176 /note= "S176R"
 FT Misc-difference 183 /note= "Q183A"
 XX
 PN WO9618648-A1.
 XX
 XX 20-JUN-1996.
 PD
 XX 13-DEC-1995; 95WO-IT000216.
 PF
 XX 14-DEC-1994; 94IT-RM000805.
 PR
 XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.

XX
PI Ciliberto G, Savino R, Lahm A, Toniatti C;
XX WPI; 1996-300575/30.
XX
XX Identifying interleukin-6 super-agonists and (super)antagonists - using a
PT 3-dimensional model of bovine granulocyte colony stimulating factor to
PT identify binding sites.
XX
XX Claim 8; Page ?; 26pp; English.
XX
XX AAW02610-W02612 represent human interleukin-6 (IL-6) mutants (see
CC AAW02609 for wild type sequence), with an increased specificity for the
CC specific receptor. These sequences were identified using the method of
CC the invention. The method comprises comparing IL-6 with the sequence of
CC the bovine granulocyte colony stimulating factor (bG-CSF). On the basis
CC of this comparison a 3-dimensional model of IL-6 is formulated, which
CC allows the identification of residues that form the site of interaction
CC with the specific receptor, and those that constitute the site of
CC interaction with gp130. The method can be used to identify superagonists,
CC antagonists, and superantagonists of IL-6. The IL-6 superagonists
CC identified by this method can be used for the treatment of
CC thrombocytopenia, and for the ex vivo expansion of human haematopoietic
CC progenitor cells for bone marrow transplantation and gene therapy. They
CC can also be used for the treatment of breast cancer, leukaemia, and
CC infectious diseases or diseases connected with disorders of bone marrow
CC progenitor cells. The antagonists and superantagonists identified by the
CC method (see AAW08476-W08478) can be used for the treatment of diseases
CC characterised by the overproduction of IL-6, particularly multiple
CC myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
CC lupus erythematosus. The method can also be used to identify IL-6
CC variants with a greater affinity for the specific receptor, or variants
CC with a reduced or abolished affinity for gp130. (Updated on 25-MAR-2003
CC to correct PR field.)
XX
XX Sequence 184 AA;
XX
XX *Query Match 17.2%; Score 188; DB 2; Length 184;
Best Local Similarity 26.2%; Pred. No. 5.9e-13;
Matches 43; Conservative 38; Mismatches 83; Indels 0; Gaps 0;
QY 28 PEFKDLIIQRLNWMWVDECDFRDLVYRTGCKGILEPAAIFHLKLPAINDTDHCGLIG 87
DB 18 PLTSSERIDKQIRYILDGISALRKETCNKSNWCESSKEALAENNLNPKMAEKDCYFIG 77
QY 88 FNETSLCKLADGFFEFVFLFKLTTEFGKSVINVDVNMELTKTLGWDIQEELNKLTKTH 147
DB 78 FNEETCLVKIITGLLEFEVLYLQNRPFESSEBQARAVQMTKVLQFLQKAKNLDALT 137
QY 148 YSPPKFDRGLLGRLOGLKYVVRHFASFYVLSAMEKFAQAVRVL 191
DB 138 TPDPTNASLLTKQAQNOQLQDMTTHLIRSFKEFLIRSLAL 181
RESULT 6
AAW02610
ID AAW02610 standard; protein; 184 AA.
XX
XX AAW02610;
XX
XX 25-MAR-2003 (revised)
DT 24-FEB-1997 (first entry)
XX
XX Interleukin-6 (Q75Y, S76I, Q175I, S176R, Q183A).
XX
XX Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
KW bovine; granulocyte colony stimulating factor; bG-CSF; receptor; gp130;
KW thrombocytopenia; haematopoietic progenitor cell; rheumatoid arthritis;
KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
XX
XX Homo sapiens.
XX

XX
FH Key Location/Qualifiers
FT Misc-difference 75 /note= "Q75Y"
FT
FT Misc-difference 76 /note= "S76I"
FT Misc-difference 175 /note= "Q175I"
FT Misc-difference 176 /note= "S176R"
FT Misc-difference 183 /note= "Q183A"
FT
XX W09618648-A1.
PN 20-JUN-1996.
PD
XX 13-DEC-1995; 95WO-IT000216.
PF
XX 14-DEC-1994; 94IT-RM000805.
PR
XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
PA
XX Ciliberto G, Savino R, Lahm A, Toniatti C;
PI
XX WPI; 1996-300575/30.
DR
XX Identifying interleukin-6 super-agonists and (super)antagonists - using a
PT 3-dimensional model of bovine granulocyte colony stimulating factor to
PT identify binding sites.
XX
XX Claim 8; Page ?; 26pp; English.
XX
XX AAW02610-W02612 represent human interleukin-6 (IL-6) mutants (see
CC AAW02609 for wild type sequence), with an increased specificity for the
CC specific receptor. These sequences were identified using the method of
CC the invention. The method comprises comparing IL-6 with the sequence of
CC the bovine granulocyte colony stimulating factor (bG-CSF). On the basis
CC of this comparison a 3-dimensional model of IL-6 is formulated, which
CC allows the identification of residues that form the site of interaction
CC with the specific receptor, and those that constitute the site of
CC interaction with gp130. The method can be used to identify superagonists,
CC antagonists, and superantagonists of IL-6. The IL-6 superagonists
CC identified by this method can be used for the treatment of
CC thrombocytopenia, and for the ex vivo expansion of human haematopoietic
CC progenitor cells for bone marrow transplantation and gene therapy. They
CC can also be used for the treatment of breast cancer, leukaemia, and
CC infectious diseases or diseases connected with disorders of bone marrow
CC progenitor cells. The antagonists and superantagonists identified by the
CC method (see AAW08476-W08478) can be used for the treatment of diseases
CC characterised by the overproduction of IL-6, particularly multiple
CC myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
CC lupus erythematosus. The method can also be used to identify IL-6
CC variants with a greater affinity for the specific receptor, or variants
CC with a reduced or abolished affinity for gp130. (Updated on 25-MAR-2003
CC to correct PR field.)
XX
XX Sequence 184 AA;
XX
XX Query Match 17.1%; Score 187; DB 2; Length 184;
Best Local Similarity 26.2%; Pred. No. 7.5e-13;
Matches 43; Conservative 38; Mismatches 83; Indels 0; Gaps 0;
QY 28 PEFKDLIIQRLNWMWVDECDFRDLVYRTGCKGILEPAAIFHLKLPAINDTDHCGLIG 87
DB 18 PLTSSERIDKQIRYILDGISALRKETCNKSNWCESSKEALAENNLNPKMAEKDCYFIG 77
QY 88 FNETSLCKLADGFFEFVFLFKLTTEFGKSVINVDVNMELTKTLGWDIQEELNKLTKTH 147
DB 78 FNEETCLVKIITGLLEFEVLYLQNRPFESSEBQARAVQMTKVLQFLQKAKNLDALT 137
QY 148 YSPPKFDRGLLGRLOGLKYVVRHFASFYVLSAMEKFAQAVRVL 191

D_b 138 TPDPTNASLLTKLQANQWLQDMTHLILRSFKEFLIRSLRAL 181

RESULT 7

ADL89593
ID ADL89593 standard; protein; 183 AA.

XX
AC ADL89593;

DT 03-JUN-2004 (first entry)

DE Human modified cytokine protein #875.

Human, cytokine; proteolysis; interferon; IFN; interleukin-10; IL-10; long-chain cytokine family; short-chain cytokine family; infection; allergy; heart disease; cancer; liver disorder; autoimmune disease; growth disorder; diabetes; neurodegenerative disease; antimicrobial; antiallergic; cystostatic; immunosuppressive; antidiabetic; neuroprotective; mutant; mutagen.

OS Homo sapiens.
OS Synthetic.

XX PN WO2004022593 -

XX
XX
XXXXX

PD 18-MAR-2004.

08-SEP-2003; 2003WO-IB004347.

XX
PR 09-SEP-2002; 2002US-0409898P.
DD 21-MAR-2002; 2002US-0457125P.

PR 21-MAR-2003; 2003US-045/135P.
XX (NAUT-) NAUTILUS BIOTECH
PA

FA (NAUT- / NAUTILEUS BIOIECH;
XX

PI Gantier R, Guyon T, Vega M, Drittanti L;

DR WPI; 2004-248447/23.

PT New modified cytokines with increased resistance to proteolysis, useful
PT for diagnosing and treating diseases such as infections, allergies, heart
PT diseases, cancer, liver disorders, autoimmune diseases or diabetes.

PS Disclosure; SEQ ID NO 927; 316pp; English.

The invention relates to modified cytokines that exhibit increased resistance to proteolysis compared to unmodified cytokines. The invention also relates to nucleic acid molecules encoding the cytokines, a pharmaceutical composition comprising a nucleic acid molecule in a pharmaceutical carrier, and a method of generating a protein or peptide molecule having a predetermined property or activity, or a pre-selected altered phenotype. The modified cytokine is selected from a member of the interferons (IFNs)/interleukin (IL)-10 protein family, a member of the long-chain cytokine family or a member of the short-chain cytokine family. The composition and method are useful for diagnosing and treating diseases such as infections, allergies, heart diseases, cancer, liver disorders, autoimmune diseases, growth disorders, diabetes or neurodegenerative diseases. This sequence represents a human modified cytokine protein of the invention.

Sequence 183 AA;

Query Match 17.0%; Score 186; DB 8; Length 183;

Best Local Similarity 26.2%; Pred. No. 9.7e-13;

Matches 43; Conservative 37; Mismatches 84; Indels 0; Gaps 0;

QY 28 PEFKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINTDHCLIG 87

17 BITSEEPINVOIPVITDCISAIPEKTCNKSNMCESSKEAI AENNINIPYMAEKDCCESSC 76

09 ENETSCU KYI AOCSEEEBUD EKEI TTTECKSVINIMIMEI I TKTU CWDIOEEI NYI TKTU 14

QY 88 FNETSCLRKRLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKH I4


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Matches 43; Conservative 36; Mismatches 85; Indels 0; Gaps 0;
QY 28 PFEEKDLLQRLNWMLWVIDECERDLCTGTGCKGILEPAAIFHLKLPAINDTDCGLIG 87
Db 17 PLTSSRIDQIRYIILDGIGSALRKETCNKSNMCSSKEALAENNLNLPKIAEKDGCQFSG 76
QY 88 FNETSKLKLADGFFEFVFLKPLTTFEGKSVINVDVWELLTKTLGWDIOBELNKLTKTH 147
Db 77 FNEETCLVKIITGLLEFFVLEVLQNRFSSEBQARAVQMTKVLQIQLQKKAKNLDAIT 136
QY 148 YSPPKFDRGLGRLOGLKLYVVRHFASFYVLSAMEKFAGQAVRVL 191
Db 137 TDPPTTINASLLTKQAQNLQMDMTTHILRSFKFLOSSLRAL 180

RESULT 12
AAP81162
ID AAP81162 standard; protein; 201 AA.
XX
AC AAP81162;
XX
XX 25-MAR-2003 (revised)
DT 15-OCT-1990 (first entry)
XX
XX Polypeptide with B-cell differentiation factor (BCDF) activity.
XX
XX B-cell differentiation factor; BCDF; cancer; autoimmune.
XX
XX Homo sapiens.
XX
XX EP257406-A.
XX
XX 02-MAR-1988.
XX
XX 06-AUG-1987; 87EP-00111409.
XX
XX 06-AUG-1986; 86JP-00184858.
XX
XX 27-AUG-1986; 86JP-00200433.
XX
XX 18-DEC-1986; 86JP-00302699.
XX
XX 13-MAY-1987; 87JP-00116332.
XX
XX 16-NOV-1987; 87JP-00289007.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX Kishimoto T, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
XX
XX WPI; 1988-057698/09.
XX
XX Purified polypeptide with B-cell differentiation factor activity -
XX
XX useful in prodn. of antibodies for diagnosis and therapy of cancers,
XX
XX infectious diseases etc.
XX
XX Claim 12; Page 41; 72pp; English.
XX
XX Peptide with BCDF activity may be used in the production and repair of B-
XX
XX cells, it is useful in treatment of autoimmune diseases, malignant tumors
XX
XX and may be used to influence B-cells to produce Abs in vitro. (Updated on
XX
XX 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
XX
XX field.)
XX
XX Sequence 201 AA;
XX
XX Query Match 16.8%; Score 184; DB 1; Length 201;
XX
XX Best Local Similarity 28.1%; Pred. No. 1.9e-12;
XX
XX Matches 41; Conservative 31; Mismatches 74; Indels 0; Gaps 0;
QY 46 IDECFRDLCTGTGCKGILEPAAIFHLKLPAINDTDCGLIGFNETSKLKLADGFFEP 105
Db 53 IDKLKRETCNKNMCSSKEALAENNLNLPKIAEKDGCQFSGFBETCLVKITGLLEFE 112
QY 106 VLFKFLTTFEGKSVINVDVWELLTKTLGWDIOBELNKLTKTHYSPPKFDRLGLGRLOGLK 165
Db 113 VYLEVLQNRFSSEBQARAVQMTKVLQIQLQKKAKNLDAITTPDPTTINASLLTKQAQ 172
```

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QY 166 YVVRHFASFYVLSAMEKFAGQAVRVL 191
Db 173 QWLQDMTTHILRSFKFLOSSLRAL 198

RESULT 13
AAU9248
ID AAU9248 standard; protein; 212 AA.
XX
AC AAU9248;
XX
XX 24-SEP-2002 (first entry)
XX
XX Human interleukin-6, IL6, variant #4.
XX
XX Human; interleukin-6; IL6; myeloma; arthritis; CAD; Kaposi sarcoma;
XX
XX coronary artery disease; inflammatory cytokine; hypercalcaemia;
XX
XX bone disease; inflammatory disease; HIV;
XX
XX human immunodeficiency virus infection; stunted growth; isogene;
XX
XX systemic onset juvenile chronic arthritis; haplotype; genotype;
XX
XX chromosome 7p21-p15; gene therapy; SNP; single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 31 /note= "Wild-type Pro substituted by Thr"
XX
XX WO200238586-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US047077.
XX
XX 09-NOV-2000; 2000US-0247578P.
XX
XX 21-AUG-2001; 2001US-0313963P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Bentivegna SC, Bieglecki KM, Chew A, Denton RR, Lachowicz M;
XX
XX Mandabalan K, Parks KE, Sausker EA;
XX
XX WPI; 2002-519290/55.
XX
XX Genetic variants of interleukin-6 isogenes for improving efficiency and
XX
XX reliability in drug development for treating myeloma, coronary artery
XX
XX disease, arthritis and Kaposi sarcoma.
XX
XX Claim 29; Page; 86pp; English.
XX
XX The invention relates to a polynucleotide comprising a first nucleotide
XX
XX sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine)
XX
XX isogene selected from isogenes 1-11 and 13-18 given in the specification,
XX
XX where each isogene comprises the regions of NS1 and is further defined by
XX
XX the corresponding sequence of polymorphisms whose locations and
XX
XX identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17),
XX
XX or a second nucleotide sequence (NS2) complementary to NS1.
XX
XX Alternatively, the sequence comprises a coding sequence for an IL6
XX
XX isogene. Also included are methods of haplotyping/ genotyping (and
XX
XX predicting the haplotype/genotype) of the IL6 gene of an individual,
XX
XX identifying an association between a trait and at least one haplotype or
XX
XX haplotype pair of the IL6 gene, an isolated oligonucleotide for detecting
XX
XX a polymorphism in the IL6 gene, a recombinant non-human organism (III)
XX
XX transformed or transfected with the IL6 polynucleotide, an isolated
XX
XX fragment of the IL6 isogene comprising at least 10 and containing one of
XX
XX the identified single- nucleotide polymorphisms (SNP), an isolated
XX
XX polypeptide (or fragment) comprising an amino acid sequence which is a
XX
XX polymorphic variant of IL6, an isolated monoclonal antibody specific for
XX
XX IL6, a computer system for storing and analysing polymorphism data for
XX
XX the IL6 gene, and a genome anthology for the IL6 gene. The IL6
XX
XX polymorphic variant is useful in screening for drugs targeting IL6 that
XX
XX are useful for treating myeloma, coronary artery disease (CAD),
```

CC arthritis, Kaposi sarcoma (associated with human immunodeficiency virus
CC infection, HIV), hypercalcaemia, bone disease, inflammatory disease,
CC stunted growth and systemic onset juvenile chronic arthritis. The methods
CC are useful for improving the efficiency and reliability in the discovery
CC and development of drugs and in the validation of IL6 as a drug target.
CC The antibody is useful in diagnostic, prognostic and therapeutic methods.
CC The IL6 isogene is useful in studying the expression and function of IL6,
CC and in expressing IL6 protein for use in screening for candidate drugs.
CC The gene for IL6 is located on chromosome 7p21-p15. The present sequence
CC is an interleukin-6 protein variant. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the IL6
CC sequence appearing as AAU99244 and the information on page 29
XX Sequence 212 AA;
SQ

Query Match 16.8%; Score 184; DB 5; Length 212;
Best Local Similarity 25.8%; Pred. No. 2e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LQLRNWMLWVDECFRDLCYRT 57
Db 16 LGLLLVLPAAFPAPVTPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGIGALKETCNKS 75
Qy 58 GICKGILEPAALPHLKLPAINDTHCGLIGFNETSCLKLDGFFFEVLFKELTTFEGK 117
Db 76 NMCESSKEALAENNLNLPKAEKDGCGFSGFNEETCLVKITGLLEFEVLEYLQNRFS 135
Qy 118 SVINVDVMEILLTKLWDIOBELNKLTKHYSPPKFDRGLLGRLOGLUKYVVRHFASPYVL 177
Db 136 SEEQARAVQMSKVLQFLQKAKNLDALTTPDPTTNASLLTKLQAOQNQLQDMTHLIL 195
Qy 178 SAMEKFAQAVRVL 191
Db 196 RSPKEFLQSSLRAL 209

RESULT 14
AAU99249
ID AAU99249 standard; protein; 212 AA.
XX
AC AAU99249;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human interleukin-6, IL6, variant #5.
XX

KW Human; interleukin-6; IL6; myeloma; arthritis; CAD; Kaposi sarcoma;
KW coronary artery disease; inflammatory cytokine; hypercalcaemia;
KW bone disease; inflammatory disease; HIV;
KW human immunodeficiency virus infection; stunted growth; isogene;
KW systemic onset juvenile chronic arthritis; haplotype; genotype;
KW chromosome 7p21-p15; gene therapy; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FH Misc-difference 31
FT /note= "Wild-type Pro substituted by Thr"
FT Misc-difference 162
FT /note= "Wild-type Asp substituted by Glu"
XX
XX WO200238586-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US047077.
XX
XX 09-NOV-2000; 2000US-0247578P.
XX 21-AUG-2001; 2001US-0313963P.
XX
XX (GENA-) GENAISANCE PHARM INC.
XX
XX Bentivegna SC, Bieglecki KM, Chew A, Denton RR, Lachowicz M;

PI Nandabalan K, Parks KB, Sausker EA;
XX WPI; 2002-519290/55.
XX
XX Genetic variants of interleukin-6 isogenes for improving efficiency and
XX reliability in drug development for treating myeloma, coronary artery
XX disease, arthritis and Kaposi sarcoma.
XX Claim 29; Page; 86pp; English.
XX

CC The invention relates to a polynucleotide comprising a first nucleotide
CC sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine)
CC isogene selected from isogenes 1-11 and 13-18 given in the specification,
CC where each isogene comprises the regions of NS1 and is further defined by
CC the corresponding sequence of polymorphisms whose locations and
CC identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17),
CC or a second nucleotide sequence (NS2) complementary to NS1.
CC Alternatively, the sequence comprises a coding sequence for an IL6
CC isogene. Also included are methods of haplotyping/ genotyping (and
CC predicting the haplotype/genotype) of the IL6 gene of an individual,
CC identifying an association between a trait and at least one haplotype or
CC haplotype pair of the IL6 gene, an isolated oligonucleotide for detecting
CC a polymorphism in the IL6 gene, a recombinant non-human organism (III)
CC transformed or transfected with the IL6 polynucleotide, an isolated
CC fragment of the IL6 isogene comprising at least 10 and containing one of
CC the identified single- nucleotide polymorphisms (SNP), an isolated
CC polypeptide (or fragment) comprising an amino acid sequence which is a
CC polymorphic variant of IL6, an isolated monoclonal antibody specific for
CC IL6, a computer system for storing and analysing polymorphism data for
CC the IL6 gene, and a genome anthology for the IL6 gene. The IL6
CC polymorphic variant is useful in screening for drugs targeting IL6 that
CC are useful for treating myeloma, coronary artery disease (CAD),
CC arthritis, Kaposi sarcoma (associated with human immunodeficiency virus
CC infection, HIV), hypercalcaemia, bone disease, inflammatory disease,
CC stunted growth and systemic onset juvenile chronic arthritis. The methods
CC are useful for improving the efficiency and reliability in the discovery
CC and development of drugs and in the validation of IL6 as a drug target.
CC The antibody is useful in diagnostic, prognostic and therapeutic methods.
CC The IL6 isogene is useful in studying the expression and function of IL6,
CC and in expressing IL6 protein for use in screening for candidate drugs.
CC The gene for IL6 is located on chromosome 7p21-p15. The present sequence
CC is an interleukin-6 protein variant. Note: The present sequence is not
CC shown in the specification but was created by the indexer using the IL6
CC sequence appearing as AAU99244 and the information on page 29
XX
XX Sequence 212 AA;
SQ

Query Match 16.8%; Score 184; DB 5; Length 212;
Best Local Similarity 25.8%; Pred. No. 2e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LQLRNWMLWVDECFRDLCYRT 57
Db 16 LGLLLVLPAAFPAPVTPGDSKDVAAAPHRQPLTSSERIDKQIRYILDGIGALKETCNKS 75
Qy 58 GICKGILEPAALPHLKLPAINDTHCGLIGFNETSCLKLDGFFFEVLFKELTTFEGK 117
Db 76 NMCESSKEALAENNLNLPKAEKDGCGFSGFNEETCLVKITGLLEFEVLEYLQNRFS 135
Qy 118 SVINVDVMEILLTKLWDIOBELNKLTKHYSPPKFDRGLLGRLOGLUKYVVRHFASPYVL 177
Db 136 SEEQARAVQMSKVLQFLQKAKNLEAITTPDPTTNASLLTKLQAOQNQLQDMTHLIL 195
Qy 178 SAMEKFAQAVRVL 191
Db 196 RSPKEFLQSSLRAL 209

RESULT 15
AAU99250
ID AAU99250 standard; protein; 212 AA.
XX
AC AAU99250;

24-SEP-2002 (first entry)
Human interleukin-6, IL6, variant #6.

Human; interleukin-6; IL6; myeloma; arthritis; CAD; Kaposi sarcoma; coronary artery disease; inflammatory cytokine; hypercalcaemia; bone disease; inflammatory disease; HIV; human immunodeficiency virus infection; stunted growth; isogene; systemic onset juvenile chronic arthritis; haplotype; genotype; chromosome 7p21-p15; gene therapy; SNP; single nucleotide polymorphism.

Homo sapiens.

Key Location/Qualifiers
Misc-difference 31 /note= "Wild-type Pro substituted by Thr"
Misc-difference 32 /note= "Wild-type Pro substituted by Ser"

WO200238586-A2.
16-MAY-2002.
09-NOV-2001; 2001WO-US047077.
09-NOV-2000; 2000US-0247578P.
21-AUG-2001; 2001US-0313963P.
(GENA-) GENAISSANCE PHARM INC.
Bentivegna SC, Bieglecki KM, Chew A, Denton RR, Lachowicz M; Nandabalan K, Parks KE, Sausker EA;
WPI; 2002-519290/55.

Genetic variants of interleukin-6 isogenes for improving efficiency and reliability in drug development for treating myeloma, coronary artery disease, arthritis and Kaposi sarcoma.

Claim 29; Page: 86pp; English.

The invention relates to a polynucleotide comprising a first nucleotide sequence (NS1) comprising a IL6 (interleukin-6, an inflammatory cytokine) isogene selected from isogenes 1-11 and 13-18 given in the specification, where each isogene comprises the regions of NS1 and is further defined by the corresponding sequence of polymorphisms whose locations and identities are defined in the specification (PS2-PS6, PS8 and PS10-PS17), or a second nucleotide sequence (NS2) complementary to NS1.

Alternatively, the sequence comprises a coding sequence for an IL6 isogene. Also included are methods of haplotyping/ genotyping (and predicting the haplotype/genotype) of the IL6 gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the IL6 gene, an isolated oligonucleotide for detecting a polymorphism in the IL6 gene, a recombinant non-human organism (III) transformed or transfected with the IL6 polynucleotide, an isolated fragment of the IL6 isogene comprising at least 10 and containing one of the identified single- nucleotide polymorphisms (SNP), an isolated polypeptide (or fragment) comprising an amino acid sequence which is a polymorphic variant of IL6, an isolated monoclonal antibody specific for IL6, a computer system for storing and analysing polymorphism data for the IL6 gene, and a genome anthology for the IL6 gene. The IL6 polymorphic variant is useful in screening for drugs targeting IL6 that are useful for treating myeloma, coronary artery disease (CAD), arthritis, Kaposi sarcoma (associated with human immunodeficiency virus infection, HIV), hypercalcaemia, bone disease, inflammatory disease, stunted growth and systemic onset juvenile chronic arthritis. The methods are useful for improving the efficiency and reliability in the discovery and development of drugs and in the validation of IL6 as a drug target. The antibody is useful in diagnostic, prognostic and therapeutic methods. The IL6 isogene is useful in studying the expression and function of IL6, and in expressing IL6 protein for use in screening for candidate drugs. The gene for IL6 is located on chromosome 7p21-p15. The present sequence

CC is a interleukin-6 protein variant. Note: The present sequence is not shown in the specification but was created by the indexer using the IL6 CC sequence appearing as AAU99244 and the information on page 29

XX
SQ Sequence 212 AA;
Query Match 16.8%; Score 184; DB 5; Length 212;
Best Local Similarity 25.5%; Pred. No. 2e-12; Indels 8; Gaps 2;
Matches 50; Conservative 42; Mismatches 96;
QY 4 FKLWLLVGSLL-----LVSGTRGKLPDAPEF-----KDLIIQLRLNMLWVIDECFRDLCY 55
DB 14 FSLGLLLVLPRAFPAPVTSGEDSKDVAAPHRQPLTSSERIDKQIRVILDGIGALRKETCN 73
QY 56 RTGICKGILEPAAIFHLKLPAINDDTHCGLIGFNETSCILKLAGDFEFVLFKFLITTF 115
DB 74 KSNMCSSKEALAENNLNLPKMAEKDGCFOSGFNEETCLVKIITGLLEFEVYLYLQNR 133
QY 116 GKSVINVDVMEILLTKTGWDIQEELNKLTKTHYSPKFDGRGLGLQGLKYWVRHFASFY 175
DB 134 ESSSEQARAVQMSKVLQFLOKKAKNLDAITPDPTTNASLLTKLQANQWLQDMTTHL 193
QY 176 VLSAMEKFAQAVRVL 191
DB 194 ILRSFKEFLQSSLRAL 209

Search completed: March 30, 2005, 22:01:41
Job time : 227.955 secs

GenCore version 5.1.6
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OM: protein - protein search, using sw model

Run on: March 30, 2005, 21:58:00 ; Search time 53.9731 Seconds
(without alignments)
282.148 Million cell updates/sec

Title: US-10-828-343-2

Perfect score: 1095

Sequence: 1 MCWFKLWSLLVSGT.....GQAVRVLDSPDVTDPVHDX 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	3	US-09-230-637-25
2	1095	100.0	204	3	US-09-230-371A-26
3	992	90.6	185	3	US-09-122-443-16
4	992	90.6	185	4	US-09-558-089-16
5	992	90.6	185	4	US-09-558-087-16
6	992	90.6	185	4	US-09-558-474-16
7	183.5	16.8	184	2	US-08-945-529-12
8	183	16.7	185	1	US-07-918-181A-4
9	183	16.7	185	1	US-07-918-181A-8
10	183	16.7	185	1	US-08-231-575-4
11	183	16.7	185	1	US-08-231-575-8
12	183	16.7	185	5	PCT-US93-06928-4
13	183	16.7	185	5	PCT-US93-06928-8
14	183	16.7	212	1	US-08-792-0198-9
15	183	16.7	212	3	US-08-988-819-9
16	183	16.7	212	3	US-09-016-534-9
17	183	16.7	212	3	US-08-097-869-7
18	183	16.7	212	3	US-08-795-473B-6
19	183	16.7	212	3	US-09-230-637-45
20	183	16.7	212	3	US-09-155-941-1
21	183	16.7	212	3	US-09-230-371A-27
22	183	16.7	212	4	US-09-439-856-6
23	183	16.7	212	4	US-09-462-941-13
24	183	16.7	212	6	5510472-2
25	183	16.7	212	6	5510472-2
26	183	16.7	232	4	US-09-949-016-10315
27	182	16.6	184	2	US-08-693-182-2

28	182	16.6	184	2	US-09-008-482-2	Sequence 2, Appli
29	181	16.5	183	1	US-08-009-973-1	Sequence 1, Appli
30	181	16.5	184	1	US-08-567-047-2	Sequence 2, Appli
31	181	16.5	184	2	US-08-567-048-2	Sequence 2, Appli
32	181	16.5	184	6	5186931-1	Patent No. 5186931
33	181	16.5	184	6	5186931-1	Patent No. 5186931
34	181	16.5	185	1	US-07-632-070B-1	Sequence 1, Appli
35	181	16.5	185	1	US-07-918-181A-2	Sequence 2, Appli
36	181	16.5	185	1	US-07-918-181A-6	Sequence 6, Appli
37	181	16.5	185	1	US-08-231-575-2	Sequence 2, Appli
38	181	16.5	185	1	US-08-231-575-6	Sequence 6, Appli
39	181	16.5	185	1	US-08-246-427A-5	Sequence 5, Appli
40	181	16.5	185	2	US-08-716-317-7	Sequence 7, Appli
41	181	16.5	185	2	US-08-766-620-5	Sequence 5, Appli
42	181	16.5	185	5	PCT-US93-06928-2	Sequence 2, Appli
43	181	16.5	185	5	PCT-US93-06928-6	Sequence 6, Appli
44	181	16.5	185	6	5186931-2	Patent No. 5186931
45	181	16.5	185	6	5186931-2	Patent No. 5186931

ALIGNMENTS

RESULT 1

US-09-230-637-25

; Sequence 25, Application US/09230637

; Patent No. 6264958

; GENERAL INFORMATION:

; APPLICANT: Hayward, Gary

; APPLICANT: Nicholas, John

; APPLICANT: Hardwick, J. Marie

; APPLICANT: Reitz, Marvin

; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma

; FILE REFERENCE: 1107.78372

; CURRENT APPLICATION NUMBER: US/09/230, 637

; CURRENT FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: 60/022,591

; PRIOR FILING DATE: 1996-07-25

; PRIOR APPLICATION NUMBER: PCT US 97/12931

; PRIOR FILING DATE: 1997-07-24

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 204

; TYPE: PRT

; ORGANISM: Kaposi's sarcoma-associated herpes-like virus

US-09-230-637-25

Query Match 100.0%; Score 1095; DB 3; Length 204;

Best Local Similarity 100.0%; Pred. No. 3.5e-123;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MCWFKLWSLLVSGTGRGKLPDAPPEKDLLIQRLLNMLWVDECPDRDLCYRTGIC	60
Db	1	MCWFKLWSLLVSGTGRGKLPDAPPEKDLLIQRLLNMLWVDECPDRDLCYRTGIC	60
Qy	61	KGILEPAAIFHLKLPAINDTDHGCLIGFNETSCCLKADGFFFEVLFKFLTTFEGKSVI	120
Db	61	KGILEPAAIFHLKLPAINDTDHGCLIGFNETSCCLKADGFFFEVLFKFLTTFEGKSVI	120
Qy	121	NVDVMELLTKLGWDIQEELNKLTKTHYSPKPDRLGLRQGLKYVVRHFASFYVLSAM	180
Db	121	NVDVMELLTKLGWDIQEELNKLTKTHYSPKPDRLGLRQGLKYVVRHFASFYVLSAM	180
Qy	181	EKFAGQAVRVLDSPDVTDPVHDK	204
Db	181	EKFAGQAVRVLDSPDVTDPVHDK	204

RESULT 2

US-09-230-371A-26

; Sequence 26, Application US/09230371A

; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-26

Query Match 100.0%; Score 1095; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.5e-123;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCWFKLSLLVGSLLVSGTRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCTRTGIC 60
DB 1 MCWFKLSLLVGSLLVSGTRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCTRTGIC 60

QY 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFVLKFLTTEFGKSVI 120
DB 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFVLKFLTTEFGKSVI 120

QY 121 NVDMVLLTKTLGWDIQEELNKLTKTHYSPKFDRLGLRLQGLKYVVRHFPASFVYLSAM 180
DB 121 NVDMVLLTKTLGWDIQEELNKLTKTHYSPKFDRLGLRLQGLKYVVRHFPASFVYLSAM 180

QY 181 EKFAQAVRVLSIDPVDVHDK 204
DB 181 EKFAQAVRVLSIDPVDVHDK 204

RESULT 3
US-09-122-443-16
; Sequence 16, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090

; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-16

Query Match 90.6%; Score 992; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCTRTGICKGILEPAAIFHLKLPAIND 79
DB 1 TRGKLPDAPEFEKDLIIQRLNMLWVIDECFRDLCTRTGICKGILEPAAIFHLKLPAIND 60

QY 80 TDHCGLIGFNETSCLKKLADGFFEFVLKFLTTEFGKSVINVDVWELLTKTLGWDIOEE 139
DB 61 TDHCGLIGFNETSCLKKLADGFFEFVLKFLTTEFGKSVINVDVWELLTKTLGWDIOEE 120

QY 140 LNKLTHTHYPKFDRLGLRLQGLKYVVRHFPASFVYLSAMEKFAQAVRVLSIDPVDVTP 199
DB 121 LNKLTHTHYPKFDRLGLRLQGLKYVVRHFPASFVYLSAMEKFAQAVRVLSIDPVDVTP 180

QY 200 DVHDK 204
DB 181 DVHDK 185

RESULT 4
US-09-558-089-16
; Sequence 16, Application US/09558089
; Patent No. 6479634
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,089
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant

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;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-089-16

Query Match          90.6%; Score 992; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79
Db 1 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 60

Qy 80 TDHCGLIGFNETSCLKKLADGPFEPFVLFKPLTTEFGKSVINVDVMELLTKTLGWDIQEE 139
Db 61 TDHCGLIGFNETSCLKKLADGPFEPFVLFKPLTTEFGKSVINVDVMELLTKTLGWDIQEE 120

Qy 140 LNKLTHTYSPKFDRLGLRLQGLKYWRHFASFYVLSAMEKFAQAVRVLDSIPDVTP 199
Db 121 LNKLTHTYSPKFDRLGLRLQGLKYWRHFASFYVLSAMEKFAQAVRVLDSIPDVTP 180

Qy 200 DVHDK 204
Db 181 DVHDK 185

RESULT 5
US-09-558-087-16
; Sequence 16, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,087
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-087-16

Query Match          90.6%; Score 992; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79
Db 1 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 60

Qy 80 TDHCGLIGFNETSCLKKLADGPFEPFVLFKPLTTEFGKSVINVDVMELLTKTLGWDIQEE 139
Db 61 TDHCGLIGFNETSCLKKLADGPFEPFVLFKPLTTEFGKSVINVDVMELLTKTLGWDIQEE 120

Qy 140 LNKLTHTYSPKFDRLGLRLQGLKYWRHFASFYVLSAMEKFAQAVRVLDSIPDVTP 199
Db 121 LNKLTHTYSPKFDRLGLRLQGLKYWRHFASFYVLSAMEKFAQAVRVLDSIPDVTP 180

Qy 200 DVHDK 204
Db 181 DVHDK 185

RESULT 6
US-09-558-474-16
; Sequence 16, Application US/09558474
; Patent No. 6835825
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-474-16

Query Match          90.6%; Score 992; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 7e-111;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79
Db 1 TRGKLPDAPEFEXDGLLIQRLNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 60

Qy 80 TDHCGLIGFNETSCLKKLADGPFEPFVLFKPLTTEFGKSVINVDVMELLTKTLGWDIQEE 139
Db 61 TDHCGLIGFNETSCLKKLADGPFEPFVLFKPLTTEFGKSVINVDVMELLTKTLGWDIQEE 120

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[illegible]

Qy	200 DVHDK 204
Db	181 DVHDK 185

RESULT 7
US-08-945-529-12
; Sequence 12, Application US/08945529
; Patent No. 5972902
; GENERAL INFORMATION:
; APPLICANT: CILIBERTO, Gennaro
; APPLICANT: SAVINO, Rocco
; APPLICANT: PAONESSA, Giacomo
; TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
; TITLE OF INVENTION: ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
; TITLE OF INVENTION: THE PREPARATION OF PHARMACEUTICAL COMPOUNDS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRONDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

[illegible]

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db
145 ASLLTKLOAONOWLODMTTHLILRSKFELIRSLRAL 181

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1  RESULT 8
2  US-07-918-181A-4
3  Sequence 4, Application US/07918181A
4  Patent No. 5338833
5  GENERAL INFORMATION:
6  APPLICANT: Fowlkes, Dana M.
7  TITLE OF INVENTION: C-Terminal IL-6 Muteins
8  NUMBER OF SEQUENCES: 35
9  CORRESPONDENCE ADDRESS:
10 ADDRESS: Imclone Systems Incorporated
11 STREET: 180 Varick Street
12 CITY: New York
13 STATE: New York
14 COUNTRY: United States
15 ZIP: 10014
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: PatentIn Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/07/918,181A
23 FILING DATE: 23-JUL-1992
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Sheets, Eric J.
27 REGISTRATION NUMBER: 30,326
28 REFERENCE/DOCKET NUMBER: FOW-2
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 212-645-1405
31 TELEFAX: 212-645-2054
32 INFORMATION FOR SEQ ID NO: 4:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 185 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37 MOLECULE TYPE: protein
38 US-07-918-181A-4

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	Query Match	16.7%	Score 183;	DB 1;	Length 185;
	Best Local Similarity	25.6%;	Pred. No. 1e-13;		
	Matches	42;	Conservative 38;	Mismatches 84;	Indels 0; Gaps 0;
Qy	28	PEFEKDLIIQLRWMLWVIDECFRLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIG	87		
Db	19	PLTSSERIDKOIRYILDGISALRKETCNKNMCCSSKEALAENNINLPKWAOKDGCFTQSG	78		
Qy	88	FNETSCLKLAGDGFPEFEVLFKFLITTFEGKSVINVDVWMLTTTLGWDIOEELNKLTKTH	147		
Db	79	FNETCLVKIITGLLEFEVLYLVIONFFESSEBQARAVQSTKVLQLOKCAKNLDAIT	138		
Qy	148	YSPKPFDRGLLRQLGKLYWRHFASFYVLGAMEKFAQAVRVL	191		
Db	139	TPDPTTNASLTKLQAOONWLODMTTHLILRSKLKEFLOSSIRAL	182		

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RESULT 9
US-07-918-181A-8
; Sequence 8, Application US/07918181A
; Patent No. 5338833
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Muteins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
;

```

```

; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,181A
; FILING DATE: 23-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheets, Eric J.
; REGISTRATION NUMBER: 30,326
; REFERENCE/DOCKET NUMBER: FOW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-918-181A-8

Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 1e-13;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

Qy 28 PEPEKLLIQRNLNMLWVIDECPDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLG 87
Db 19 PLTSSERIDQIRYILDGISALRKETCNKSNMCESSKEALAEANNLNPMAEKDGCFCQSG 78
Qy 88 FNETSCLKLAGDGFEEFVLFKFTTTEFGKSVINVDVWMLLTGKWDIOEELNKLTKTH 147
Db 79 FNEETCLVKIITGLLEFEVLYLQNRPFESSEQARAVQMSTKVLIOFLQKAKNLDAIT 138
Qy 148 YSPKPKDRGLGLRGLQGLKYWRHFASFYVLSAMEKFAQAVRVL 191
Db 139 TPDPPTNASLLTKLAQNQLQDMTTHLILRSLEKFLQSSLRAL 182

RESULT 10
US-08-231-575-4
; Sequence 4, Application US/08231575
; Patent No. 5565336
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Muteins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,575
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/918,181
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheets, Eric J.
; REGISTRATION NUMBER: 30,326
; REFERENCE/DOCKET NUMBER: FOW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-575-8

Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 1e-13;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

Qy 28 PEPEKLLIQRNLNMLWVIDECPDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLG 87
Db 19 PLTSSERIDQIRYILDGISALRKETCNKSNMCESSKEALAEANNLNPMAEKDGCFCQSG 78
Qy 88 FNETSCLKLAGDGFEEFVLFKFTTTEFGKSVINVDVWMLLTGKWDIOEELNKLTKTH 147
Db 79 FNEETCLVKIITGLLEFEVLYLQNRPFESSEQARAVQMSTKVLIOFLQKAKNLDAIT 138
Qy 148 YSPKPKDRGLGLRGLQGLKYWRHFASFYVLSAMEKFAQAVRVL 191
Db 139 TPDPPTNASLLTKLAQNQLQDMTTHLILRSLEKFLQSSLRAL 182

RESULT 11
US-08-231-575-8
; Sequence 8, Application US/08231575
; Patent No. 5565336
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Muteins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,575
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/918,181
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheets, Eric J.
; REGISTRATION NUMBER: 30,326
; REFERENCE/DOCKET NUMBER: FOW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-575-8

Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 1e-13;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

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; REFERENCE/DOCKET NUMBER: FOW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-575-4

Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 1e-13;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

Qy 28 PEPEKLLIQRNLNMLWVIDECPDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLG 87
Db 19 PLTSSERIDQIRYILDGISALRKETCNKSNMCESSKEALAEANNLNPMAEKDGCFCQSG 78
Qy 88 FNETSCLKLAGDGFEEFVLFKFTTTEFGKSVINVDVWMLLTGKWDIOEELNKLTKTH 147
Db 79 FNEETCLVKIITGLLEFEVLYLQNRPFESSEQARAVQMSTKVLIOFLQKAKNLDAIT 138
Qy 148 YSPKPKDRGLGLRGLQGLKYWRHFASFYVLSAMEKFAQAVRVL 191
Db 139 TPDPPTNASLLTKLAQNQLQDMTTHLILRSLEKFLQSSLRAL 182

RESULT 11
US-08-231-575-8
; Sequence 8, Application US/08231575
; Patent No. 5565336
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: C-Terminal IL-6 Muteins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,575
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/918,181
; FILING DATE: 23-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheets, Eric J.
; REGISTRATION NUMBER: 30,326
; REFERENCE/DOCKET NUMBER: FOW-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-231-575-8

Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 1e-13;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

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Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
 QY 28 PFEKDLIQLRNWMLWVDECFRDLGYRTGICKGILEPAAIFHLKLPAINDTDHGCLIG 87
 DB 19 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPQWAEKDGCFQSG 78
 QY 88 FNETSCLKLAGDGFPEFVKFLTFTEFGKSVINVDVMELLTKTLGWDIOEELNKLTKTH 147
 DB 79 FNEETCLVKIITGLLEFEVLEYLQNRFFESSEQARAVQMSTKVLQIQLQKAKNLDALT 138
 QY 148 YSPPKFDRGLGRLOGLKTYVVRHFASFYVLSAMEKFAQAVRVL 191
 DB 139 TPDPTTNASLLTKLQAOQNQLQMDMTTHLILSLKFEFQSSLRAL 182

RESULT 12
 PCT-US93-06928-4
 ; Sequence 4, Application PC/TUS9306928
 ; GENERAL INFORMATION:
 ; APPLICANT: Fowlkes, Dana M.
 ; TITLE OF INVENTION: Carboxy Terminal IL-6 Muteins
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ImClone Systems Incorporated
 ; STREET: 180 Varick Street
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11014
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/06928
 ; FILING DATE: 19930723
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/918,181
 ; FILING DATE: 23-JUL-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Feit, Irving N.
 ; REGISTRATION NUMBER: 28,601
 ; REFERENCE/DOCKET NUMBER: FOW-2-T
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-645-1405
 ; TELEFAX: 212-645-2054
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 185 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US93-06928-4

Query Match 16.7%; Score 183; DB 5; Length 185;
 Best Local Similarity 25.6%; Pred. No. 1e-13;
 Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
 QY 28 PFEKDLIQLRNWMLWVDECFRDLGYRTGICKGILEPAAIFHLKLPAINDTDHGCLIG 87
 DB 19 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPQWAEKDGCFQSG 78
 QY 88 FNETSCLKLAGDGFPEFVKFLTFTEFGKSVINVDVMELLTKTLGWDIOEELNKLTKTH 147
 DB 79 FNEETCLVKIITGLLEFEVLEYLQNRFFESSEQARAVQMSTKVLQIQLQKAKNLDALT 138
 QY 148 YSPPKFDRGLGRLOGLKTYVVRHFASFYVLSAMEKFAQAVRVL 191
 DB 139 TPDPTTNASLLTKLQAOQNQLQMDMTTHLILSLKFEFQSSLRAL 182

RESULT 13
 PCT-US93-06928-8
 ; Sequence 8, Application PC/TUS9306928
 ; GENERAL INFORMATION:
 ; APPLICANT: Fowlkes, Dana M.
 ; TITLE OF INVENTION: Carboxy Terminal IL-6 Muteins
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ImClone Systems Incorporated
 ; STREET: 180 Varick Street
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 11014
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/06928
 ; FILING DATE: 19930723
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/918,181
 ; FILING DATE: 23-JUL-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Feit, Irving N.
 ; REGISTRATION NUMBER: 28,601
 ; REFERENCE/DOCKET NUMBER: FOW-2-T
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-645-1405
 ; TELEFAX: 212-645-2054
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 185 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US93-06928-8

Query Match 16.7%; Score 183; DB 5; Length 185;
 Best Local Similarity 25.6%; Pred. No. 1e-13;
 Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
 QY 28 PFEKDLIQLRNWMLWVDECFRDLGYRTGICKGILEPAAIFHLKLPAINDTDHGCLIG 87
 DB 19 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPQWAEKDGCFQSG 78
 QY 88 FNETSCLKLAGDGFPEFVKFLTFTEFGKSVINVDVMELLTKTLGWDIOEELNKLTKTH 147
 DB 79 FNEETCLVKIITGLLEFEVLEYLQNRFFESSEQARAVQMSTKVLQIQLQKAKNLDALT 138
 QY 148 YSPPKFDRGLGRLOGLKTYVVRHFASFYVLSAMEKFAQAVRVL 191
 DB 139 TPDPTTNASLLTKLQAOQNQLQMDMTTHLILSLKFEFQSSLRAL 182

RESULT 14
 US-08-792-019B-9
 ; Sequence 9, Application US/08792019B
 ; Patent No. 5741772
 ; GENERAL INFORMATION:
 ; APPLICANT: CHANG, MING-SHI
 ; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMGEN INC.
 ; STREET: 1840 DEHAVILLAND DRIVE
 ; CITY: THOUSAND OAKS
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 91320

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/792.019B
; APPLICATION NUMBER: US/08/792.019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; FEATURE:
; NAME/KEY: Region
; LOCATION: -30..0
; US-08-792-019B-9

Query Match 16.7%; Score 183; DB 1; Length 212;
Best Local Similarity 25.8%; Pred. No. 1.3e-13;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

; QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRDLCYRT 57
; Db 16 LGLLLVLPAAFPAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKS 75
; QY 58 GICKGILEPAAIFHLKLPAINDTDHCGLIGNETSCCLKLADGFEFEVLFKFLTTFEGK 117
; Db 76 NMCESSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLVQNRFES 135
; QY 118 SVINVDVWELLTKTLGWDIQEELNKLTKTHYSPKPDGRLGLRLOGLKYVWRHFPASFYVL 177
; Db 136 SEQARAVQMSKVLQIQLQKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHLIL 195
; QY 178 SAMEKFAQAVRVL 191
; Db 196 RSPKEFLQSSLRAL 209

RESULT 15
US-08-988-819-9
; Sequence 9, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; FEATURE:
; NAME/KEY: Region
; LOCATION: -30..0
; US-08-988-819-9

Query Match 16.7%; Score 183; DB 3; Length 212;
Best Local Similarity 25.8%; Pred. No. 1.3e-13;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

; QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRDLCYRT 57
; Db 16 LGLLLVLPAAFPAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYILDGISALRKETCNKS 75
; QY 58 GICKGILEPAAIFHLKLPAINDTDHCGLIGNETSCCLKLADGFEFEVLFKFLTTFEGK 117
; Db 76 NMCESSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLVQNRFES 135
; QY 118 SVINVDVWELLTKTLGWDIQEELNKLTKTHYSPKPDGRLGLRLOGLKYVWRHFPASFYVL 177
; Db 136 SEQARAVQMSKVLQIQLQKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTTHLIL 195
; QY 178 SAMEKFAQAVRVL 191
; Db 196 RSPKEFLQSSLRAL 209

Search completed: March 30, 2005, 22:11:02
Job time : 54.9731 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	186	17.0	183	16	US-10-658-834A-927	Sequence 927, Appl	
2	184	16.8	183	16	US-10-658-834A-901	Sequence 901, Appl	
3	183	16.7	183	16	US-10-658-834A-900	Sequence 900, Appl	
4	183	16.7	183	16	US-10-658-834A-918	Sequence 918, Appl	
5	183	16.7	183	16	US-10-658-834A-920	Sequence 920, Appl	
6	183	16.7	183	16	US-10-658-834A-928	Sequence 928, Appl	
7	183	16.7	212	9	US-09-854-280-14	Sequence 14, Appl	
8	183	16.7	212	9	US-09-854-208-14	Sequence 14, Appl	
9	183	16.7	212	14	US-10-039-007A-3	Sequence 3, Appl	
10	183	16.7	212	14	US-10-400-377-13	Sequence 13, Appl	
11	183	16.7	212	14	US-10-400-708-13	Sequence 13, Appl	
12	183	16.7	212	14	US-10-298-148-13	Sequence 13, Appl	
13	183	16.7	212	15	US-10-440-464-61	Sequence 61, Appl	

QY . 88 FNETSCLKKLADGFFEFELFKFLTTEFGKSVINVDVMELLTKTGLGWDIQEELNKLTKTH 14

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Db 77 FNEETCLVKIITGLLEFEVYLEYQNRFESSEQARAVQMSTKVLIQFLQKKAKNLDALT 136
QY 148 YSPPKFDRGLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLLILRSFKFQSSLRAL 180

RESULT 2
US-10-658-834A-901
; Sequence 901, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-901

Query Match 16.8%; Score 184; DB 16; Length 183;
Best Local Similarity 26.2%; Pred. No. 1.9e-12;
Matches 43; Conservative 36; Mismatches 85; Indels 0; Gaps 0;

QY 28 PEFKDLIIQRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIG 87
Db 17 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKVAEKDGCFOG 76
QY 88 FNETSCLKKLADGPFPEVLFKLTTEFGKSVINVDVMELLTKTLGWDIOBELNKLTKTH 147
Db 77 FNEETCLVKIITGLLEFEVYLEYQNRFESSEQARAVQMSTKVLIQFLQKKAKNLDALT 136
QY 148 YSPPKFDRGLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLLILRSFKFQSSLRAL 180

RESULT 3
US-10-658-834A-900
; Sequence 900, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 900
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-900

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 37; Mismatches 85; Indels 0; Gaps 0;

QY 28 PEFKDLIIQRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIG 87
Db 17 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKVAEKDGCFOG 76
QY 88 FNETSCLKKLADGPFPEVLFKLTTEFGKSVINVDVMELLTKTLGWDIOBELNKLTKTH 147
Db 77 FNEETCLVKIITGLLEFEVYLEYQNRFESSEQARAVQMSTKVLIQFLQKKAKNLDALT 136
QY 148 YSPPKFDRGLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLLILRSFKFQSSLRAL 180

RESULT 4
US-10-658-834A-918
; Sequence 918, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 918
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-918

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

QY 28 PEFKDLIIQRLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIG 87
Db 17 PLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKVAEKDGCFOG 76
QY 88 FNETSCLKKLADGPFPEVLFKLTTEFGKSVINVDVMELLTKTLGWDIOBELNKLTKTH 147
Db 77 FNEETCLVKIITGLLEFEVYLEYQNRFESSEQARAVQMSTKVLIQFLQKKAKNLDALT 136
QY 148 YSPPKFDRGLGRLOGLKYVWRHFPASFYVLSAMEKFAQAVRVL 191
Db 137 TSDPTTNASLLTKLQAQONQWLQDMTTHLLILRSFKFQSSLRAL 180

RESULT 5
US-10-658-834A-920
; Sequence 920, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
```

APPLICANT: Guyon, Thierry
APPLICANT: Dittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid
TITLE OF INVENTION: Molecules and Related Applications
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
PRIOR FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 920
LENGTH: 183
TYPE: PRT
ORGANISM: Homo sapiens
US-10-658-834A-920

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 37; Mismatches 85; Indels 0; Gaps 0;

QY 28 PEFEKLLIQLRNWMLVDECFRDLCTGICKGILEPAAIFHLKLPAINDDTHCGLIG 87
DB 17 PLTSSRIDQIRYILDGIALRKETCNKSNMCESSKEALAENNLNPKMAEKDGCQSG 76

QY 88 FNETSCLKLADGFFPEVLFKLTTFEGKSVINVDVWMLLTKYLGWDIOEELNKLTKTH 147
DB 77 FNEETCLVKIITGLLEFEVLYLQNRFSSESEQARAVQMTKVLIQFLOKKAQNLDAIT 136

QY 148 YSPKPDRLGLRGLQGLKYVVRFPASFYVLSAMEKEFAGQAVRVL 191
DB 137 TPDPTTNASLLTKQAQNLQDMTTHLIIRSFKEFLOSSLRAL 180

RESULT 6
US-10-658-834A-928
Sequence 928, Application US/10658834A
Publication No. US20040132977A1
GENERAL INFORMATION:
APPLICANT: Gantier, Rene
APPLICANT: Guyon, Thierry
APPLICANT: Dittanti, Lila
APPLICANT: Vega, Manuel
TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
TITLE OF INVENTION: Acid
FILE REFERENCE: 38751-922
CURRENT APPLICATION NUMBER: US/10/658,834A
CURRENT FILING DATE: 2003-09-08
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2003-03-21
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 1306
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 928
LENGTH: 183
TYPE: PRT
ORGANISM: Homo sapiens
US-10-658-834A-928

Query Match 16.7%; Score 183; DB 16; Length 183;
Best Local Similarity 25.6%; Pred. No. 2.5e-12;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

QY 28 PEFEKLLIQLRNWMLVDECFRDLCTGICKGILEPAAIFHLKLPAINDDTHCGLIG 87
DB 17 PLTSSRIDQIRYILDGIALRKETCNKSNMCESSKEALAENNLNPKMAEKDGCQSG 76

QY 88 FNETSCLKLADGFFPEVLFKLTTFEGKSVINVDVWMLLTKYLGWDIOEELNKLTKTH 147
DB 77 FNEETCLVKIITGLLEFEVLYLQNRFSSESEQARAVQMTKVLIQFLOKKAQNLDAIT 136

QY 148 YSPKPDRLGLRGLQGLKYVVRFPASFYVLSAMEKEFAGQAVRVL 191
DB 137 TADPTTNASLLTKQAQNLQDMTTHLIIRSFKEFLOSSLRAL 180

RESULT 7
US-09-854-280-14
Sequence 14, Application US/09854280
Patent No. US20020052027A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
FILE REFERENCE: P1381R1C2
CURRENT APPLICATION NUMBER: US/09/854,280
CURRENT FILING DATE: 2001-05-10
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 14
LENGTH: 212
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-280-14

Query Match 16.7%; Score 183; DB 9; Length 212;
Best Local Similarity 25.8%; Pred. No. 3e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVDECFRDLCTYRT 57
DB 16 LGLLVLPAPFAPVPFGEDSKDVAAPHROPLTSSERIDKQIRYILDGIALRKETCNKS 75

QY 58 GICKGILEPAAIFHLKLPAINDDTHCGLIGFNETSCILKLADGFFPEVLFKLTTFEGK 117
DB 76 NMCESSKEALAENNLNPKMAEKDGCQSGFNETCLVKIITGLLEFEVLYLQNRFS 135

QY 118 SVINVDVWMLLTKYLGWDIOEELNKLTKTHYSPKPDRLGLRGLQGLKYVVRFPASFYV 177
DB 136 SEEQARAVQMTKVLIQFLOKKAQNLDAITTPDPTTNASLLTKQAQNLQDMTTHLI 195

QY 178 SAMEKEFAGQAVRVL 191
DB 196 RSFKEFLOSSLRAL 209

RESULT 8
US-09-854-208-14
Sequence 14, Application US/09854208
Patent No. US20020106743A1
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Filvaroff, Ellen
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Li, Hanzhong
APPLICANT: Wood, William I.
TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
FILE REFERENCE: P1381-R1
CURRENT APPLICATION NUMBER: US/09/854,208

Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
 Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKS 75
 Qy 58 GICKGILEPAAIFHLKLPAINDDHCGLIGFNETSCLKLDGFFFEVLFKELTTFEGK 117
 Db 76 NMCESSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLQNRFS 135
 Qy 118 SVINVDVMELLTKTLGWIDIOEELNKLTKTHYSPKFDRLGLGRLQGLKYVVRHFASFYVL 177
 Db 136 SEQARAVQMSKVLQFLQKAKNLDAITTPDPTTNASLLTKLQAOQNQLQDMTTHLIL 195
 Qy 178 SAMEKFAQAVRVL 191
 Db 196 RSPKEFLQSSLRAL 209

RESULT 12

US-10-298-148-13
 ; Sequence 13, Application US/10298148
 ; Publication No. US20030171284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cox III, George N
 ; APPLICANT: Bolder Biotechnology, Inc.
 ; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
 ; FILE REFERENCE: 4152-1-PUS
 ; CURRENT APPLICATION NUMBER: US/10/298,148
 ; CURRENT FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: US/09/462,941
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/052,516
 ; PRIOR FILING DATE: 1997-07-14
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; TYPE: PRT
 ; LENGTH: 212
 ; ORGANISM: Homo sapiens
 US-10-298-148-13

Query Match 16.7%; Score 183; DB 14; Length 212;
 Best Local Similarity 25.8%; Pred. No. 3e-12;
 Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
 Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
 Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKS 75
 Qy 58 GICKGILEPAAIFHLKLPAINDDHCGLIGFNETSCLKLDGFFFEVLFKELTTFEGK 117
 Db 76 NMCESSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLQNRFS 135
 Qy 118 SVINVDVMELLTKTLGWIDIOEELNKLTKTHYSPKFDRLGLGRLQGLKYVVRHFASFYVL 177
 Db 136 SEQARAVQMSKVLQFLQKAKNLDAITTPDPTTNASLLTKLQAOQNQLQDMTTHLIL 195
 Qy 178 SAMEKFAQAVRVL 191
 Db 196 RSPKEFLQSSLRAL 209

RESULT 13

US-10-440-464-61
 ; Sequence 61, Application US/10440464
 ; Publication No. US20040018528A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DEPRIMO, SAMUEL
 ; APPLICANT: O'FARRELL, ANNE-MARIE
 ; APPLICANT: MORIMOTO, ALYSSA
 ; APPLICANT: SNOLICH, BEVERLY
 ; APPLICANT: MANNING, WILLIAM
 ; APPLICANT: WALTER, SARAH
 ; APPLICANT: CHERRINGTON, JULIE

; APPLICANT: SCHILLING, JIM
 ; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
 ; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
 ; FILE REFERENCE: 038602/1592
 ; CURRENT APPLICATION NUMBER: US/10/440,464
 ; CURRENT FILING DATE: 2003-05-19
 ; PRIOR APPLICATION NUMBER: 60/380,872
 ; PRIOR FILING DATE: 2002-05-17
 ; PRIOR APPLICATION NUMBER: 60/448,922
 ; PRIOR FILING DATE: 2003-02-24
 ; PRIOR APPLICATION NUMBER: 60/448,874
 ; PRIOR FILING DATE: 2003-02-24
 ; NUMBER OF SEQ ID NOS: 185
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 61
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-440-464-61

Query Match 16.7%; Score 183; DB 15; Length 212;
 Best Local Similarity 25.8%; Pred. No. 3e-12;
 Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
 Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
 Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKS 75
 Qy 58 GICKGILEPAAIFHLKLPAINDDHCGLIGFNETSCLKLDGFFFEVLFKELTTFEGK 117
 Db 76 NMCESSKEALAENNLNPKMAEKDGCQSGFNEETCLVKIITGLLEFEVLYLQNRFS 135
 Qy 118 SVINVDVMELLTKTLGWIDIOEELNKLTKTHYSPKFDRLGLGRLQGLKYVVRHFASFYVL 177
 Db 136 SEQARAVQMSKVLQFLQKAKNLDAITTPDPTTNASLLTKLQAOQNQLQDMTTHLIL 195
 Qy 178 SAMEKFAQAVRVL 191
 Db 196 RSPKEFLQSSLRAL 209

RESULT 14

US-10-773-939-13
 ; Sequence 13, Application US/10773939
 ; Publication No. US20040175356A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cox III, George N
 ; APPLICANT: Bolder Biotechnology, Inc.
 ; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
 ; FILE REFERENCE: 4152-1-PUS
 ; CURRENT APPLICATION NUMBER: US/10/773,939
 ; CURRENT FILING DATE: 2004-02-05
 ; PRIOR APPLICATION NUMBER: US/10/400,377
 ; PRIOR FILING DATE: 2003-03-26
 ; PRIOR APPLICATION NUMBER: US/09/462,941
 ; PRIOR FILING DATE: 2000-01-14
 ; PRIOR APPLICATION NUMBER: 60/052,516
 ; PRIOR FILING DATE: 1997-07-14
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 13
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-773-939-13

Query Match 16.7%; Score 183; DB 16; Length 212;
 Best Local Similarity 25.8%; Pred. No. 3e-12;
 Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
 Qy 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
 Db 16 LGLLLVLPAAFPAPVPPGDSKVAAPHROPLTSSERIDKQIRYILDGISALRKETCNKS 75

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QY 58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKKLADGFFEFVLFKFLTTERGK 117
Db 76 NNCESSEKALAENNLNLPMAEKDGCFOGFGNEETCLVKIITGLLEFEFVLEYLQNRRES 135
QY 118 SVINVDVMELLTKTGWDIQEELNKLTKTHYSPKPFDRGLLGRLOGLKYVVRHFASFYVL 177
Db 136 SEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQONQLQDMTTHLIL 195
QY 178 SAMEKFAQAVRVL 191
Db 196 RSFKEFLOSSLRAL 209
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RESULT 15
US-10-774-149-13
; Sequence 13, Application US/10774149
; Publication No. US20040175800A1
; GENERAL INFORMATION:
; APPLICANT: Cox III, George N
; APPLICANT: Bolder Biotechnology, Inc.
; TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
; FILE REFERENCE: 4152-1-PUS
; CURRENT APPLICATION NUMBER: US/10/774,149
; PRIOR FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: US/10/400,377
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: US/09/462,941
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 60/052,516
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-774-149-13
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Query Match 16.7%; Score 183; DB 16; Length 212;
Best Local Similarity 25.8%; Pred. No. 3e-12;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
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QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRLNWMWVIDECFRDLCYRT 57
Db 16 LGLLLVLPAAFPAPVPPGDSKDVAAHPHQPTSSERIDKQIRYILDGISAIRKETCNKS 75
QY 58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKKLADGFFEFVLFKFLTTERGK 117
Db 76 NNCESSEKALAENNLNLPMAEKDGCFOGFGNEETCLVKIITGLLEFEFVLEYLQNRRES 135
QY 118 SVINVDVMELLTKTGWDIQEELNKLTKTHYSPKPFDRGLLGRLOGLKYVVRHFASFYVL 177
Db 136 SEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQONQLQDMTTHLIL 195
QY 178 SAMEKFAQAVRVL 191
Db 196 RSFKEFLOSSLRAL 209
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Search completed: March 30, 2005, 22:09:56
Job time : 173.897 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:47:50 ; Search time 48.4843 Seconds
(without alignments)
404.837 Million cell updates/sec

Title: US-10-828-343-2
Perfect score: 1095
Sequence: 1 MCWFKLWSLLVGSLLVSGT.....GQAVRVLDSPDVTDPVHDK 204
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	183	16.7	212	1 IVHUB2	interleukin-6 prec
2	180.5	16.5	212	2 I46590	interleukin 6 - pi
3	179.5	16.4	212	2 I46621	prointerleukin 6 -
4	173.5	15.8	208	2 T09216	interleukin-6 prec
5	150	13.7	208	1 S29549	interleukin-6 - sh
6	148	13.5	211	1 ICMS6	interleukin-6 prec
7	143.5	13.1	208	1 A56610	interleukin-6 prec
8	134	12.2	211	2 A34247	interleukin-6 prec
9	128	11.7	207	2 I46084	interleukin 6 - ca
10	92.5	8.4	873	2 E90581	hypothetical prote
11	86.5	7.9	487	2 H69472	coenzyme F420-quin
12	85	7.8	408	2 A56186	cyclin E - African
13	83	7.6	626	2 AG1523	DNA primase [impor
14	82.5	7.5	447	1 UBMBJM	tubulin beta-1 cha
15	82.5	7.5	449	2 QJ1589	tubulin beta-5 cha
16	82.5	7.5	969	2 T41707	probable pheromone
17	82	7.5	367	2 T18185	probable site-spec
18	82	7.5	626	2 AC1619	DNA primase [impor
19	81.5	7.4	442	2 S00683	tubulin beta-1 cha
20	80.5	7.4	449	2 QJ1591	tubulin beta-7 cha
21	80	7.3	874	2 AB0385	probable polysacch
22	80	7.3	955	2 F84372	valine-CRNA ligase
23	79.5	7.3	451	2 S50748	beta-tubulin - pot
24	79.5	7.3	452	2 S50748	beta-tubulin - pot
25	79.5	7.3	1017	2 S67804	LRG1 protein - yea
26	79	7.2	385	2 T27626	hypothetical prote
27	78.5	7.2	445	2 JA0048	tubulin beta-1 cha
28	78.5	7.2	674	2 T19495	hypothetical prote
29	77.5	7.1	609	2 S04757	NADH2 dehydrogenas

30	77.5	7.1	771	2 S51421	hypothetical prote
31	77	7.0	1004	2 B69483	hypothetical prote
32	77	7.0	1810	2 T30562	resistance protein
33	76.5	7.0	447	2 S17729	tubulin beta chain
34	76.5	7.0	447	2 S17730	tubulin beta chain
35	76.5	7.0	461	2 T39889	protein kinase - f
36	76	6.9	1005	2 B82969	sarcosine oxidase
37	75.5	6.9	164	2 T32824	hypothetical prote
38	75.5	6.9	260	2 D64246	DNA-directed DNA p
39	75.5	6.9	602	2 C72043	DNA gyrase, chain
40	75.5	6.9	602	2 H86579	DNA gyrase subunit
41	75.5	6.9	1158	2 T50454	probable rhoI GDP-
42	75	6.8	172	2 A46695	epididymal secreto
43	75	6.8	244	2 E72364	ABC transporter, A
44	75	6.8	333	2 B64380	hypothetical prote
45	75	6.8	505	1 S19169	cytochrome P450 2D

ALIGNMENTS

RESULT 1

IVHUB2

Interleukin-6 precursor [validated] - human

N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell

on factor

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004

C;Accession: A32648; A25692; A26966; A3515; A25801; A25921; I52193; I56003; A27601; B27

R;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muracani, K.; Matsuda, T.; Nakai, S.; Kishimoto

EMBO J. 6, 2939-2945, 1987

A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene

A;Reference number: A32648; MUID:88082664; PMID:3500852

A;Accession: A32648

A;Molecule type: DNA

A;Residues: 1-212 <YAS>

A;Cross-references: UNIPROT:P05231; GB:X00081; NID:G29494; PIDN:CAA68278.1; PID:G29495

A;Note: the authors translated the codon CAG for residue 130 as Glu

R;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.

EMBO J. 5, 2529-2537, 1986

A;Title: Structure and expression of cDNA and genes for human interferon-beta-2, a disti

A;Reference number: A91051; MUID:87053818; PMID:3023045

A;Accession: A25692

A;Molecule type: mRNA

A;Residues: 1-212 <ZIL>

A;Cross-references: GB:X04430; NID:G32673; PIDN:CAA28026.1; PID:G32674

R;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura

i, T.; Kishimoto, T.

Nature 324, 73-76, 1986

A;Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocy

A;Reference number: A93387; MUID:87065033; PMID:3491322

A;Accession: A26966

A;Molecule type: mRNA

A;Residues: 1-212 <HIR>

A;Cross-references: NID:G33849; PIDN:CAA28268.1; PID:G33850

R;Tonouchi, N.; Miwa, K.; Kasayama, H.; Matsui, H.

Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989

A;Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of

A;Reference number: A33515; MUID:89391958; PMID:2789513

A;Accession: A33515

A;Molecule type: mRNA

A;Residues: 1-212 <TON>

A;Cross-references: NID:G186349; PIDN:AAA59154.1; PID:G307063

R;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.

Eur. J. Biochem. 159, 625-632, 1986

A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h

A;Reference number: A25801; MUID:87004683; PMID:3758081

A;Accession: A25801

A;Molecule type: DNA: mRNA

A;Residues: 1-212 <HAE>

A;Cross-references: GB:X04403

A;Experimental source: fibroblast

R;May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A>Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433; PMID:3538015
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAY>
 A:Cross-references: GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
 R:Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Mitt. 83, 40-47, 1988
 A>Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: I52193; MUID:89193317; PMID:3266463
 A:Accession: I52193
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <WON>
 A:Cross-references: GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910
 R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A>Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
 A:Reference number: I56003; MUID:88088768; PMID:3320204
 A:Accession: I56003
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BRA>
 A:Cross-references: GB:M18403; NID:g184631; PIDN:AAA52729.1; PID:g306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A>Title: Separation and comparison of two monokines with lymphocyte-activating factor activity
 A:Reference number: A29816; MUID:88154445; PMID:3279116
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VAN1>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved in cell growth and differentiation
 A:Reference number: A60400; MUID:90171574; PMID:2307841
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <VAM>
 R:Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and its cDNA
 A:Reference number: A29085; MUID:87092370; PMID:3491991
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Aizawa, H.
 Anticancer Res. 11, 961-968, 1991
 A>Title: Purification and characterization of human fibroblast derived differentiation factor
 A:Reference number: A61159; MUID:91290785; PMID:1640338
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NOD>
 A:Experimental source: fibroblast
 R:Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A>Title: Interleukin 6 is the principal cytokine in the differentiation of human interleukin-6 dependent cell lines
 A:Reference number: A61462; MUID:90121567; PMID:2610854
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriske, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A>Title: Marked cell-type-specific differences in glycosylation of human interleukin-6
 A:Reference number: A48419; MUID:91355644; PMID:1883960
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAY2>
 A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
 A>Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form contained only N-linked carbohydrate
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAY3>
 A:Experimental source: FS-4 fibroblasts
 A>Note: sequence extracted from NCBI backbone (NCBIP:63787)
 A>Note: this 23-25K form contained O-linked but not N-linked carbohydrate
 R:Orlita, T.; Oneda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 produced in *Escherichia coli*
 A:Reference number: JX0305; MUID:94266765; PMID:8206884
 A:Accession: JX0305
 A>Status: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human interleukin-6 are similar to those of human granulocyte colony-stimulating factor
 A:Reference number: S04981; MUID:89286115; PMID:2472117
 A:Accession: S04981
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044; PMID:8172889
 A:Accession: A54253
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factors and cytokines. It therefore appears to function as an autoregulator of cell growth and differentiation. It therefore appears to function as an autoregulator of cell growth and differentiation. It therefore appears to function as an autoregulator of cell growth and differentiation.
 C:Comment: This protein plays a regulatory role in various host defense mechanisms and in the regulation of the immune response.
 C:Genetics: GDB:IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growth factor; interleukin-6; signal sequence; status predicted <SIG>
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 F:30-212/Product: interleukin-6, short form; status experimental <MATS>
 F:72-78, 101-111/Disulfide bonds: #status experimental
 F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
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Query Match	16.7%	Score 183;	DB 1;	Length 212;
Best Local Similarity	25.8%	Pred. No. 5.5e-10;		
Matches	50;	Conservative 38;	Mismatches 9;	Indels 14; Gaps 2;
QY	12	VGSLVSGTRGKLPDAP-EFEKDL	-----LIQRINWMLWVIDEFCRDLCYRT	57
Db	16	LGLLVLPAPPAVPVPPGDSKDVAAHPHQPLTSSRIDKQIRYILDGIALRKETCNKS	75	
QY	58	GICKGILEPAAIFHLKLPAINDTDHCGLIGNETSKLADGFEFEVLPKFLTFEGK	117	
Db	76	NMCSSKEALANNLNPMAEKDGCQSGFNEETCLVKIITGLLEFVYLEYLQNRFPES	135	
QY	118	SVINVDVMEILTKLGWDIQBELNKLTKTHYSPPKFDRGLLRQLGKLVVRRHFAFVYL	177	
Db	136	SEEQARAVQMSTKVLQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNLQDMTHLL	195	
QY	178	SAMEKFAQAVRVL	191	
Db	196	RSFKEFLQSSLRAL	209	

RESULT 2
 I46590
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A>Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conceptuses
 A:Reference number: I46590; MUID:92360284; PMID:1497880
 A:Accession: I46590

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:g164514; PID:g164515
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6

Query Match 16.4%; Score 179.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 9.5e-09;
Matches 48; Conservative 49; Mismatches 79; Indels 25; Gaps 4;

QY 12 VGSLLVSGTRGKLPDAPPE-----KGLPD-----APPEKDLLLQRLNMLWVIDECFRDL 53
Db 16 LGLLVWATAFPTTGRLEEDAKGATSDKMLFTSPDKTEEL-----IKYILGKISAMRKEM 71

QY 54 CYRTGICKGILEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKFLTT 113
Db 72 CEKYEKENSKEVLAENNLNPKMAEKDGCFCQSGFNQETCLMRITGLVFEQIYLDYLOK 131

QY 114 EFKSVINVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 173
Db 132 EYESKGNVEAVQISTKALITQLRQKGNPKDATTNPNTNAGLLDKLQSQNEMWKNTKI 191

QY 174 FYVLNAME---KFAQQAVRVL 191
Db 192 ILILSLDFLOFSLRAIRIM 212

RESULT 4
T09216
interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M86722; NID:g164624; PID:g164625
C;Genetics:
A;Gene: IL6
C;Superfamily: interleukin-6

Query Match 16.4%; Score 179.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 1.2e-09;
Matches 48; Conservative 49; Mismatches 79; Indels 25; Gaps 4;

QY 12 VGSLLVSGTRGKLPDAPPE-----KGLPD-----APPEKDLLLQRLNMLWVIDECFRDL 53
Db 16 LGLLVWATAFPTTGRLEEDAKGATSDKMLFTSPDKTEEL-----IKYILGKISAMRKEM 71

QY 54 CYRTGICKGILEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKFLTT 113
Db 72 CEKYEKENSKEVLAENNLNPKMAEKDGCFCQSGFNQETCLMRITGLVFEQIYLDYLOK 131

QY 114 EFKSVINVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 173
Db 132 EYESKGNVEAVQISTKALITQLRQKGNPKDATTNPNTNAGLLDKLQSQNEMWKNTKI 191

QY 174 FYVLNAME---KFAQQAVRVL 191
Db 192 ILILSLDFLOFSLRAIRIM 212

RESULT 4
T09216
interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:g164514; PID:g164515
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6

Query Match 16.5%; Score 180.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 9.5e-10;
Matches 47; Conservative 46; Mismatches 87; Indels 17; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAPPE-----KDLLLQRLNMLWVIDECFRDL 57
Db 16 LGLLVWATAFPTTGRLEEDAKGATSDKMLFTSPDKTEELIKYILGKISAMRKEMCEKY 75

QY 58 GICKGILEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKFLTTFFGK 117
Db 76 EKENSKEVLAENNLNPKMAEKDGCFCQSGFNQETCLMRITGLVFEQIYLDYLOKYES 135

QY 118 SVINVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 177
Db 136 NKGNEAVQISTKALITQLRQKGNPKDATTNPNTNAGLLDKLQSQNEMWKNTKIIL 195

QY 178 SAME---KFAQQAVRVL 191
Db 196 RSLEDFLOFSLRAIRIM 212

RESULT 3
I46621
prointerleukin 6 - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46621
R;Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A;Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of
A;Reference number: I46621; MUID:91338547; PMID:1873476
A;Accession: I46621
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <RIC>
A;Cross-references: UNIPROT:P26893; GB:M86722; NID:g164624; PID:g164625
C;Genetics:
A;Gene: IL6
C;Superfamily: interleukin-6

Query Match 16.4%; Score 179.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 1.2e-09;
Matches 48; Conservative 49; Mismatches 79; Indels 25; Gaps 4;

QY 12 VGSLLVSGTRGKLPDAPPE-----KGLPD-----APPEKDLLLQRLNMLWVIDECFRDL 53
Db 16 LGLLVWATAFPTTGRLEEDAKGATSDKMLFTSPDKTEEL-----IKYILGKISAMRKEM 71

QY 54 CYRTGICKGILEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKFLTT 113
Db 72 CEKYEKENSKEVLAENNLNPKMAEKDGCFCQSGFNQETCLMRITGLVFEQIYLDYLOK 131

QY 114 EFKSVINVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 173
Db 132 EYESKGNVEAVQISTKALITQLRQKGNPKDATTNPNTNAGLLDKLQSQNEMWKNTKI 191

QY 174 FYVLNAME---KFAQQAVRVL 191
Db 192 ILILSLDFLOFSLRAIRIM 212

RESULT 4
T09216
interleukin-6 precursor - horse
C;Species: Equus caballus (domestic horse)

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-212 <MAT>
A;Cross-references: UNIPROT:P26893; GB:M80258; NID:g164514; PID:g164515
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6

Query Match 15.8%; Score 173.5; DB 2; Length 208;
Best Local Similarity 26.0%; Pred. No. 4.3e-09;
Matches 51; Conservative 37; Mismatches 89; Indels 19; Gaps 5;

QY 12 VGSLLVSGTRGKLP-----DAPEFEKDLII-----QRLNMLWVIDECFRDL 60
Db 16 LGLLVWATAFPTTGRLEEDAKGATSDKMLFTSPDKTEELIKYILGKISAMRKEMCNFSKC 75

QY 61 KGLEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKFLTTFFGKSVI 120
Db 76 ENSKEVLAENNLNPKMAEKDGCFCQSGFNQETCLMRITGLSEFQIYLDYLOKFEKGEKE 135

QY 121 NVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 178
Db 136 NIKTMQISTKVL---VOILMQKNPEVTTPDTAKSSLLAKLHSONEWLKNKTTTHILR 192

QY 179 AME---KFAQQAVRVL 191
Db 193 SLEDFLOFSLRAIRIM 208

RESULT 5
S29549
interleukin-6 - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S29549
R;Ebrahim, B.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S29549
A;Accession: S29549
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-208 <EBR>
A;Cross-references: UNIPROT:P29455; EMBL:X68723
C;Superfamily: interleukin-6

Query Match 13.7%; Score 150; DB 1; Length 208;
Best Local Similarity 27.0%; Pred. No. 7.7e-07;
Matches 38; Conservative 28; Mismatches 71; Indels 4; Gaps 1;

QY 51 RDLCTGTCGKILEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKF 110
Db 69 KEICEKNDCEKSKETLAENKLPKMEKDCGFCQSGFNQAVCLITTAGLLBYQIYLD 128

QY 111 LTTEFGKSVINVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 170
Db 129 LQNEPEGNQETVMELQSSIRTLLIQLKEKIAGLIIT---PATHTDLLEKMQSSNEWKN 184

QY 171 FASFYVLNAMEKFPAGQAVRVL 191
Db 185 AKVILIILSRLENFLQFRLRAI 205

RESULT 6
ICMS6
interleukin-6 precursor - mouse
N;Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatoc

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09216
R;Swiderski, C.E.; Horohov, D.W.
Submitted to the EMBL Data Library, July 1996
A;Reference number: Z16613
A;Accession: T09216
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-208 <SWI>
A;Cross-references: UNIPROT:Q95181; EMBL:U64794; NID:g2654387; PID:g2654388
C;Genetics:
A;Gene: IL-6
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor

Query Match 15.8%; Score 173.5; DB 2; Length 208;
Best Local Similarity 26.0%; Pred. No. 4.3e-09;
Matches 51; Conservative 37; Mismatches 89; Indels 19; Gaps 5;

QY 12 VGSLLVSGTRGKLP-----DAPEFEKDLII-----QRLNMLWVIDECFRDL 60
Db 16 LGLLVWATAFPTTGRLEEDAKGATSDKMLFTSPDKTEELIKYILGKISAMRKEMCNFSKC 75

QY 61 KGLEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKFLTTFFGKSVI 120
Db 76 ENSKEVLAENNLNPKMAEKDGCFCQSGFNQETCLMRITGLSEFQIYLDYLOKFEKGEKE 135

QY 121 NVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 178
Db 136 NIKTMQISTKVL---VOILMQKNPEVTTPDTAKSSLLAKLHSONEWLKNKTTTHILR 192

QY 179 AME---KFAQQAVRVL 191
Db 193 SLEDFLOFSLRAIRIM 208

RESULT 5
S29549
interleukin-6 - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S29549
R;Ebrahim, B.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S29549
A;Accession: S29549
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-208 <EBR>
A;Cross-references: UNIPROT:P29455; EMBL:X68723
C;Superfamily: interleukin-6

Query Match 13.7%; Score 150; DB 1; Length 208;
Best Local Similarity 27.0%; Pred. No. 7.7e-07;
Matches 38; Conservative 28; Mismatches 71; Indels 4; Gaps 1;

QY 51 RDLCTGTCGKILEPAAIFHLKLPAINDTDHGCLIGFNETSCLKLAGDGFPEFVLFKF 110
Db 69 KEICEKNDCEKSKETLAENKLPKMEKDCGFCQSGFNQAVCLITTAGLLBYQIYLD 128

QY 111 LTTEFGKSVINVDVMBELLTKTLGWDIOEELNKLTKTHYSPPKFDRGLLGRLOGLKYVVRH 170
Db 129 LQNEPEGNQETVMELQSSIRTLLIQLKEKIAGLIIT---PATHTDLLEKMQSSNEWKN 184

QY 171 FASFYVLNAMEKFPAGQAVRVL 191
Db 185 AKVILIILSRLENFLQFRLRAI 205

RESULT 6
ICMS6
interleukin-6 precursor - mouse
N;Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatoc

acytoma growth factor
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
 C:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S10
 J.Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
 J. Immunol. 141, 3875-3881, 1988
 A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
 A:Reference number: A30531; MUID:89035525; PMID:3263439
 A:Accession: A30531
 A:Molecule type: DNA
 A:Residues: 1-211 <TAN>
 A:Cross-references: UNIPROT:P08505; GB:M20572; NID:G198369; PIDN:AAA39302.1; PID:G387386
 R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim
 Eur. J. Immunol. 18, 193-197, 1988
 A:Title: cDNA cloning of murine interleukin-HP1: homology with human interleukin 6.
 A:Reference number: A27610; MUID:88166883; PMID:2965020
 A:Accession: A27610
 A:Molecule type: mRNA
 A:Residues: 1-211 <VAN>
 A:Cross-references: GB:X06203; NID:G52701; PIDN:CAA29560.1; PID:G52702
 R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla
 J. Immunol. 142, 1372-1376, 1989
 A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
 A:Reference number: A30571; MUID:89124383; PMID:2563387
 A:Accession: A30571
 A:Molecule type: mRNA
 A:Residues: 5-211 <MOC>
 A:Cross-references: GB:M24221; NID:G341131; PIDN:AA68814.1; PID:G870699
 R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
 Eur. J. Biochem. 176, 187-197, 1988
 A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
 A:Reference number: S01323; MUID:88229059; PMID:3262059
 A:Accession: S01323
 A:Molecule type: protein
 A:Residues: 25-166, 'X', 168-211 <SIM>
 A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
 R:Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
 Nucleic Acids Res. 18, 6455, 1990
 A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
 A:Reference number: S12103; MUID:91057159; PMID:2243807
 A:Accession: S12103
 A:Molecule type: mRNA
 A:Residues: 1-211 <GRE>
 A:Cross-references: EMBL:X54542; NID:G52727; PIDN:CAA38411.1; PID:G52728
 R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
 Biochem. Biophys. Res. Commun. 166, 139-145, 1990
 A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
 A:Reference number: A90157; MUID:90147691; PMID:2302197
 A:Accession: E34047
 A:Molecule type: protein
 A:Residues: 66-69, 'X', 71-75; 78-94; 128-148 <JAS>
 R:Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simp
 Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokin
 A:Reference number: A26662; MUID:87092311; PMID:2948184
 A:Accession: A26662
 A:Molecule type: protein
 A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
 R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clon
 A:Reference number: A40486; MUID:89017145; PMID:3262872
 A:Accession: A40486
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHI>
 A:Cross-references: GB:J03783; NID:G198367; PIDN:AAA39301.1; PID:G309410
 R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
 Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Reference number: A60799; MUID:89062753; PMID:3264198
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHA>

R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mol
 A:Reference number: S10241; MUID:90171860; PMID:2108569
 A:Accession: S10241
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:G49738; PIDN:CAA35824.1; PID:G5981860
 R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the tryptophan residues in murine interleukin-
 A:Reference number: S38254; MUID:94039075; PMID:8223586
 A:Accession: S38254
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 38-60, 75, 'X', 77-79; 176-203 <ZHA>
 C:Genetics:
 A:Gene: IL-6
 A:Map position: 5
 A:Introns: 7/1, 68/3; 106/3; 156/3
 C:Superfamily: interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; a
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-211/Product: interleukin-6 #status experimental <MAT>
 Query Match 13.5%; Score 148; DB 1; Length 211;
 Best Local Similarity 24.5%; Pred. No. 1.2e-06;
 Matches 47; Conservative 35; Mismatches 96; Indels 14; Gaps 3;
 QY 12 VGSLLVSGT-----RGKL-----PDAPFEKDLIIQLRNWMLWVIDECFRDLCYRTG 58
 DB 15 LGLMLVTTTAPTTSQVRGDFTEDTNRPVYTSQVGLTHVLWEIVEMKELCNGNS 74
 QY 59 ICKGILEPAAIFHLKLPAINDTDHGGLIGFNETCLKXKLADGFFEFVFLKPLTFE- GK 117
 DB 75 DQNNDDALAENLKLPEIQNRDGCYQGYNQEIQLKISSGLLEYHSYLEYMKNNLKD 134
 QY 118 SVINVDVVELLTITLGDWIDIQSELNKLTKTHYSPKFDRLGLGRLOGLKYVWRHFASFVYL 177
 DB 135 KDKARVLQRTDTLTHIFNQEVKDLHKVILPTFISNALLTDKLESQKEWLRTKTQIFIL 194
 QY 178 SAMEKFAQAVR 189
 DB 195 KSLBEFLKVTLR 206
 RESULT 7
 A56610
 Interleukin-6 precursor - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: A56610; S22162
 R:Droogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
 DNA Seq. 2, 411-413, 1992
 A:Title: Nucleotide sequence of bovine interleukin-6 cDNA.
 A:Reference number: A56610; MUID:93076003; PMID:1446077
 A:Accession: A56610
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-208 <DRO>
 A:Cross-references: UNIPROT:P26892; EMBL:X57317; NID:G2193; PIDN:CAA40572.1; PID:G2194
 A:Experimental source: BLV induced B cell-lymphosarcoma
 A:Note: sequence extracted from NCBI backbone (NCBI:P118917)
 C:Superfamily: interleukin-6
 C:Keywords: cytokine
 Query Match 13.1%; Score 143.5; DB 1; Length 208;
 Best Local Similarity 24.4%; Pred. No. 3.2e-06;
 Matches 42; Conservative 37; Mismatches 86; Indels 7; Gaps 2;
 QY 20 TRGKLDPAPFEKDLIIQLRNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIND 79

```

Db 41 TPGRLTTTPEKTEALIKR---WVDKISAMRKEICEKNDECESSETLAENKLNLPKME 97
Qy 80 TDHCGLIGFNETSCCLKLADGFEFEVLKFLTEFGKSVINVDVWELLTKTLGWDIQEE 139
Db 98 KDCGFSQGFNOAICLIRTTAGLLEYQIYLDYQNEYEGNQENVRDLRKNIRTLIQLIKQK 157
Qy 140 LNKLTHTHYSPPKDRGLLGRLOGLKYVWRHFAFYVLSAMEKFAQAVRVL 191
Db 158 IADLITT-----PATNTDLLEKMOSSNEWVNAKIILIRLENLFLOFSLRAI 205

RESULT 8
A34247
Interleukin-6 precursor - rat
N;Alternate names: IL-6
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34247
R;Northmann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A;Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derive
A;Reference number: A34247; MUID:89380206; PMID:2789217
A;Accession: A34247
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-211 <NOR>
A;Cross-references: UNIPROT:P20607; GB:M26744; NID:G204915; PIDN:AAA77659.1; PID:G204916
C;Superfamily: interleukin-6
C;Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 12.2%; Score 134; DB 2; Length 211;
Best Local Similarity 23.7%; Pred. No. 2.6e-05;
Matches 47; Conservative 34; Mismatches 91; Indels 26; Gaps 4;

Qy 12 VGSLLVSGT-----RGKLPDAPEFEKLLIQR-----DFTEDTHNRPVYTSQVGLITYVIRELEMRKE 52
Db 15 LGLMLLTATAPFTSQVRRG-----DFTEDTHNRPVYTSQVGLITYVIRELEMRKE 68

Qy 53 LCYRTGICKGILEPAALFHLKLPAINDTDHGGLIGFNETSCCLKLADGFEFEVLKFLT 112
Db 69 LCNGNSDCNMSDDALSNNLKLPEIQNRDGCFTGYNQEIQLLKI CSGLLEFRPYLEFVK 128

Qy 113 TEF-GKSVINVDVWELLTKTLGWDIQBELNKLTKHTHYSPPKDRGLLGRLOGLKYVWRHF 171
Db 129 NNLDQNKDKARVQTSNTELVHIFKQEI KDSYKIVLPTPTSNALLMEKLESQEWLRTK 188

Qy 172 ASFYVLSAMEKFAQAVR 189
Db 189 TIQLIKALBEFLKVWTR 206

RESULT 9
I46084
Interleukin 6 - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I46084
R;Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A;Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
A;Reference number: I46084; MUID:94052249; PMID:8234373
A;Accession: I46084
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-207 <BRA>
A;Cross-references: UNIPROT:P41683; GB:L16914; NID:G438519; PIDN:AAA16620.1; PID:G438520
C;Superfamily: interleukin-6

Query Match 11.7%; Score 128; DB 2; Length 207;
Best Local Similarity 27.8%; Pred. No. 9.7e-05;
Matches 42; Conservative 29; Mismatches 62; Indels 18; Gaps 5;

Qy 4 FKLMSLLLV-----GSLLVSGTRGKLPDAPEPEKDLIIQLNMLWVIDECFRDLCYR 56

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Db 14 FSIGLLLVWATAPPTPGPLGGDATSNRLPLTP---ADKMEELIKYILGKISALKKEMCDN 70
Qy 57 TGICGILSPAAALFHLKLPAINDTDHGGLIGFNETSCCLKLADGFEFEVLKFLTTEF- 115
Db 71 YNKCEDSKAALNNLNPKLAEDKCGFQSGFNQETCLIRITTTGLQEFQIYLVFLQDKYE 130
Qy 116 -----GKSV-INVDVWELLTKTLGWDIQBEL 140
Db 131 GDKENAKSVYVTSNTNVLLQMLKRRKGKN-QDEV 160

RESULT 10
E90581
hypothetical protein MYPU_5570 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90581
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90581
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-873 <KUR>
A;Cross-references: UNIPROT:Q98Q12; GB:AL445566; PID:G14089972; PIDN:CAC13730.1; GSPDB:G
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_5570
A;Genetic code: SGC3
C;Superfamily: alanyl-tRNA ligase

Query Match 8.4%; Score 92.5; DB 2; Length 873;
Best Local Similarity 24.3%; Pred. No. 1.3;
Matches 50; Conservative 27; Mismatches 58; Indels 61; Gaps 9;

Qy 32 KDLIIQLNMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHGGLIGFNET 91
Db 305 RDVYIIRL-----IRRAYRTGILQIGKDEAFLYKL-VPVIKDS----LIFDYDT 348

Qy 92 SCLKLADGFEFEVLK-----KELTFEFGKSVINVDVWELLTKTLGWDIQ----- 137
Db 349 ---KHVAKVIKDELLFELTIDQKKILEKFEKSKKIDASIVFRMPDITGYVPVETKEM 405

Qy 138 -----EELNKLTKHTHYSPPKDRG-----LLGRLOGLKYVWRHFAFYVLSAMEKFAQAVR 177
Db 406 AKEKGEISLEEFKRYQHEHLSKSKKGDGMKVINFLANIDKKVDFVGYDTLETTSK 465

Qy 178 -----SAMEKFAQAVRVLDSIP 195
Db 466 ILYLFNSESCKLNKLEGQYFILDKTP 491

RESULT 11
H69477
coenzyme F420-quinone oxidoreductase (EC 1.6.5.-) 53.9K chain AF1825 [similarity] - Arch-
N;Alternate names: F420H2-quinone oxidoreductase, 53.9K subunit nuoM homolog
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69477
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.;
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69477
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-487 <KLE>

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Db 255 AVNLPPRLHFFWVGAPLTSRGSQQYISLTVPFLTQQM--WD 296

RESULT 15

JQ1589
tubulin beta-5 chain - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: JQ1589
R:Snustad, D.P.; Haas, N.A.; Koczak, S.D.; Silflow, C.D.
Plant Cell 4, 549-556, 1992
A:Title: The small genome of Arabidopsis contains at least nine expressed beta-tubulin genes
A:Reference number: JQ1587; MUID:92361268; PMID:1496609
A:Accession: JQ1589
A:Molecule type: DNA
A:Residues: 1-449 <SNU>
A:Cross-references: UNIPROT:P29513; GB:M84702; NID:g166901; PIDN:AAA32883.1; PID:g166902
C:Genetics:
A:Gene: TUB5
C:Superfamily: tubulin
C:Keywords: microtubule

Query Match 7.5%; Score 82.5; DB 2; Length 449;
Best Local Similarity 23.8%; Pred. No. 5.3;
Matches 39; Conservative 21; Mismatches 49; Indels 55; Gaps 8;

Qy 12 VGSLLVSGTRGKLPD-----APEFEKDLIIQRLNWLWV-----IDEC----- 49
Db 148 MGTLLISKIREEYDWMLTFSVPSPKV-SDTVVEPNATLSVHQLVNADECMVLDNE 206
Qy 50 -FRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSC-----LKKL 97
Db 207 ALYDICFT-----LKLSTPSFGDLNHLISATMSGVTCSLRFPQLNSDLRKL 254
Qy 98 ADGFFFEVLKFE-----LTTERGKSVINVDVWELLTKILGWD 135
Db 255 AVNLPPRLHFFWVGAPLTSRGSQQYISLTVPFLTQQM--WD 296

Search completed: March '30, 2005, 22:06:42
Job time : 50.4843 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:12:44 ; Search time 214.063 Seconds
(without alignments)
488.007 Million cell updates/sec

Title: US-10-828-343-2
Perfect score: 1095
Sequence: 1 MCWFKWLSLLVSGT.....GQAVRVLDSPDVTDPVHDX 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	2	Q98823 human herpe
2	1095	100.0	204	2	Q768K3 human herpe
3	1088	99.4	204	2	O40918 human herpe
4	185	16.9	212	1	IL6_MACFA
5	184	16.8	212	2	Q8MKH0 macaca fasc
6	183	16.7	212	1	Q8MKH0 saimiri sci
7	183	16.7	212	1	IL6_CERTO
8	182	16.6	209	2	Q9TTH3 homo sapien
9	181	16.5	212	1	IL6_HUMAN
10	180.5	16.5	212	1	IL6_MACMU
11	179	16.3	209	2	IL6_PIG
12	177.5	16.2	212	2	Q97540 actus nancy
13	173.5	15.8	208	1	Q8MJ75 sus scrofa
14	163.5	14.9	208	1	IL6_HORSE
15	162	14.8	211	1	IL6_FELCA
16	160	14.6	214	2	Q8MKES felis silve
17	159.5	14.6	209	1	IL6_LAMGL
18	158	14.4	208	2	Q8MKES lama glama
19	158	14.4	211	2	Q8MKES sus scrofa
20	155.5	14.2	205	1	IL6_PHOVI
21	155	14.2	241	2	Q90Y10 phoca vitul
22	154.5	14.1	207	2	Q9MYZ7 canis fami
23	152	13.9	208	1	IL6_CAPHI
24	150	13.7	208	1	IL6_SHEEP
25	148	13.5	211	1	IL6_MOUSE
26	144.5	13.2	207	1	IL6_CANFA
27	143.5	13.1	208	1	IL6_BOVIN
28	143	13.1	175	2	Q9TTH4 canis fami
29	139.5	12.7	208	2	Q6V919 actus nigri
30	138	12.6	207	2	Q9JHH3 bubalus bub
31	136.5	12.5	207	2	Q28403 marmota mon
					Q28403 enhydra lut

32	135	12.3	207	1	IL6_MARMO
33	134	12.2	211	1	IL6_RAT
34	132.5	12.1	191	2	O6QHV3 marmota mon
35	132	12.1	160	2	O97535 cervus elap
36	129.5	11.8	210	2	O97535 aotus vocif
37	123.5	11.3	212	2	Q9WVQ8 mesocricetu
38	119.5	10.9	125	1	IL6_MUSVI
39	116.5	10.6	241	2	Q9MZR1 sigmodon hi
40	103.5	9.5	108	2	Q9BDL5 mustela vis
41	100.5	9.2	186	2	Q9BDL5 phocenoide
42	96.5	8.8	399	2	O6P257 meriones un
43	96	8.8	692	2	Q6N3M6 rhodopsu
44	95.5	8.7	690	2	O6DIH6 xenopus tro
45	95	8.7	684	1	CPSC_BOVIN
					Q6DRG6 brachydanio
					P79101 bos taurus

ALIGNMENTS

RESULT 1					
Q98823	ID	Q98823	PRELIMINARY;	PRT;	204 AA.
AC	Q98823;				
DT	01-FEB-1997	(TREMBlrel. 02, Created)			
DT	01-FEB-1997	(TREMBlrel. 02, Last sequence update)			
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)			
DE	Interleukin-6 homolog (fragment).				
GN	Name=VIL-6;				
OS	Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus)				
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;				
OC	Gammaherpesvirinae; Rhadinovirus.				
OX	NCBI_TaxID=37296;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,				
RA	Friedman-Kien A.-E., Fleckenstein B.;				
RT	"Human herpesvirus 8 encodes a homologue of interleukin-6.";				
RL	J. Virol. 0:0-0(1996).				
DR	EMBL	U73655	AAB18244.1;	-	
DR	PDB	1IIR	X-ray	B=-	
DR	GO	GO:0005576	C:extracellular	IEA.	
DR	GO	GO:0005125	F:cytokine activity	IEA.	
DR	GO	GO:0005138	F:interleukin-6 receptor binding	IEA.	
DR	GO	GO:0006955	P:immune response	IEA.	
DR	InterPro	IPR009079	4 helix cytokine.		
DR	InterPro	IPR003573	IL6 MGF_GCSF.		
DR	InterPro	IPR003574	Interleukin_6.		
DR	Pfam	PF00489	IL6; 1.		
DR	PRINTS	PR00433	IL6GCSFMGF.		
DR	PRINTS	PR00434	INTERLEUKIN6.		
DR	ProDom	PD004356	Interleukin_6; 1.		
DR	SMART	SM00126	IL6; 1.		
FT	NON_TER 204				
SQ	SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;				
Query Match 100.0%; Score 1095; DB 2; Length 204;					
Best Local Similarity 100.0%; Pred. No. 2.4e-92;					
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MCWFKWLSLLVSGT	TRGKLPDAPFEKDLIIQRLNMLWVIDECFRDLCYRTGIC		
Db	1	MCWFKWLSLLVSGT	TRGKLPDAPFEKDLIIQRLNMLWVIDECFRDLCYRTGIC		
Qy	61	KGILEPAAIFHLKLPAINDTDCGLIGNETSKKLADGFFFEVLFKPLTFTEFGKSVI			
Db	61	KGILEPAAIFHLKLPAINDTDCGLIGNETSKKLADGFFFEVLFKPLTFTEFGKSVI			
Qy	121	NVDVMELLTKLGWDIQEELNKLTKTHYSPKPKDRCGLGLGRLOGLKYWVRHFASFYVLSAM			
Db	121	NVDVMELLTKLGWDIQEELNKLTKTHYSPKPKDRCGLGLGRLOGLKYWVRHFASFYVLSAM			
Qy	181	EKFAGQAVRVLDSPDVTDPVHDK	204		

181 EKFAGQAVRVLSIDFVDTVDHDK 204

Db

RESULT 2

Q76SK3

ID Q76SK3 PRELIMINARY; PRT; 204 AA.

AC Q76SK3;

DT 05-JUL-2004 (TEMBLrel. 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

DE OSF K2; functional interleukin-6 vIL-6 homolog (Putative interleukin 6).

DE OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae; Rhadinovirus.

OX NCBI_TaxID=37296;

RN [1]

RN SEQUENCE FROM N.A.

RN MEDLINE=97184526; PubMed=9032328;

RX Nicholas J., Ruvoilo V., Zong J., Ciuffo D., Guo H.G., Reitz M.S.,

RA Hayward A.G.S.;

RA "A single 13-kilobase divergent locus in the Kaposi sarcoma-associated

RT herpesvirus (human herpesvirus 8) genome contains nine open reading

RT frames that are homologous to or related to cellular proteins.";

RL J. Virol. 71:1963-1974 (1997).

RN [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=97208913; PubMed=9055855;

RA Nicholas J., Ruvoilo V.R., Burns W.H., Sandford G., Wan X., Ciuffo D.,

RA Hendrickson S.B., Guo H.G., Hayward G.S., Reitz M.S.;

RT "Kaposi's sarcoma-associated human herpesvirus-8 encodes homologues of

RT macrophage inflammatory protein-1 and interleukin-6.";

RL Nat. Med. 3:287-292 (1997).

RN [3]

RN SEQUENCE FROM N.A.

RX Sun R., Lin S.-F., Miller G.;

RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RN SEQUENCE FROM N.A.

RX MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739;

RE Moore P.S., Boshoff C., Weiss R.A., Chang Y.;

RT "Molecular mimicry of human cytokine and cytokine response pathway

RT genes by KSHV.";

RL Science 274:1739-1744 (1996).

RN [5]

RN SEQUENCE FROM N.A.

RX MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;

RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,

RA Russo J.J., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;

RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;

RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus

RT (HHV8).";

RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867 (1996).

RN [6]

RN SEQUENCE FROM N.A.

RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,

RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U67774; AAB61701.1; -.

DR EMBL; U71365; AAC34937.1; -.

DR EMBL; U75698; AAC57089.1; -.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005125; F:cytokine activity; IEA.

DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.

DR GO; GO:0006355; P:immune response; IEA.

DR InterPro; IPR009079; 4 Helix cytokine.

DR InterPro; IPR003573; IL6 MGF GCFS.

DR InterPro; IPR003574; Interleukin_6.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GSEMGF.

DR PRINTS; PR00434; INTERLEUKIN_6.

DR ProDom; PD004356; INTERLEUKIN_6. 1.

DR SMART; SM00126; IL6; 1.

DR SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;

Db 1 MCWFKLSLLVSGTRGKLPDAPPEFEKOLLIQRLNMLWVIDECFRDLCTRTGIC 60
61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKLADGFFEFEVLFKFLTTTFGKSVI 120
61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKLADGFFEFEVLFKFLTTTFGKSVI 120
Qy 121 NVDVWELLTKTLGWDIOBELNKLTKTHYSPKFPDRGLLGRLOGLKYVVRHFPASFYVLSAM 180
Db 121 NVDVWELLTKTLGWDIOBELNKLTKTHYSPKFPDRGLLGRLOGLKYVVRHFPASFYVLSAM 180
Qy 181 EKFAQAVRLDSTPDVTPDVHDK 204
Db 181 EKFAQAVRLDSTPDVTPDVHDK 204

RESULT 4
IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
EP Tatsumi M.;
RA "Molecular cloning and expression of cynomolgus monkey interleukin-6."
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL CC
CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological functions: it plays an essential role in the final differentiation of B-cells into Ig-secreting cells, it induces myeloma and plasmacytoma growth, it induces nerve cells differentiation, in hepatocytes it induces acute phase reactants (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC EMBL; AB000554; BAA19148.1; -.
DR HSPP; P05231; IL6.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBFB0389 CRC64;

Query Match 16.9%; Score 185; DB 1; Length 212;

Best Local Similarity 26.3%; Pred. No. 8.2e-09;
Matches 51; Conservative 36; Mismatches 93; Indels 14; Gaps 2;
Qy 12 VGSLLVSGTRGKLPDAP-BPEKDL-----LIQRLNMLWVIDECFRDLCTVRT 57
Db 16 LGLLLVLPAAFPAPVLPGEDSKDVAAPHSPQLTSSESRIDKHRYILDGISALRKETCNRS 75
Qy 58 GICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKLADGFFEFEVLFKFLTTTFGK 117
Db 76 NMCSSKEALAEANLNLPKMAEKDGCFCQSGFNEDTCLVKIITGLLEFEVLYEQNRFES 135
Qy 118 SVINVDVWELLTKTLGWDIOBELNKLTKTHYSPKFPDRGLLGRLOGLKYVVRHFPASFYV 177
Db 136 SEQARAVQVMTKVLQFLQKAKNLDAITPTTNPASLLTKLQAOQNLQDQMTTHLIL 195
Qy 178 SAMEKFAQAVRVL 191
Db 196 RSPKFEFLOSSRLAL 209
RESULT 5
Q8MKHO PRELIMINARY; PRT; 212 AA.
AC Q8MKHO;
DT 01-OCT-2002 (T-REMBLrel. 22, Created)
DT 01-OCT-2002 (T-REMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-REMBLrel. 26, Last annotation update)
DE Interleukin-6.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
OX NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-Y;
RA Heraud J.M., Lavergne A., Kazanji M.;
RT "Molecular cloning, characterization, and quantification of squirrel monkey (Saimiri sciureus) Th1 and Th2 cytokines."
RL Immunogenetics 54:20-29(2002).
DR EMBL; AP294757; AAK92044.1; -.
DR HSPP; P05231; IL6.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23581 MW; FF22CBF493245479 CRC64;
Query Match 16.8%; Score 184; DB 2; Length 212;
Best Local Similarity 25.5%; Pred. No. 1e-08;
Matches 50; Conservative 40; Mismatches 98; Indels 8; Gaps 2;
Qy 4 FKLWSLLVLSL-----LVSGTRGKLPDAPPEFEKDLIQRLNMLWV----IDECFRDLCT 55
Db 14 FSLGLLVMPAAFPAPVTLGEDSKDVAAPNRLTLSTSTDKHWTYLDGIALRKELCN 73
Qy 56 RTGICGILEPAAIFHLKLPAINDTDHCGLIGFNETSCCLKLADGFFEFEVLFKFLTTTF 115
Db 74 KSNMCSSKEALAEANLNLPKMAEKDGCFCQSGFNEDTCLVKIITGLLEFEVLYEQNRF 133
Qy 116 GKSVINVDVWELLTKTLGWDIOBELNKLTKTHYSPKFPDRGLLGRLOGLKYVVRHFPASFY 175
Db 134 ESSKEQAGAVQVMTKVLQFLQKAKNLDAITPTTNPASLLTKLQAOQNLQDQMTTHL 193
Qy 176 VLSAMEKFAQAVRVL 191


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Db 16 LGLLLVLPAAFPAPVPBGSDSKDAVAPHRQPLTSSERIDKQIRYILDGISALRKETCNKS 75
QY 58 GICKGILEPAAIFHLKLPAINDTDHGILGFNETSCIKKLADGFFFEVLFKFLTTERGK 117
Db 76 NNCSSKEALAEENLNLPKWAEGKCGFQSGFNEETCLVKIITGLLEFEVLYLQNRFPES 135
QY 118 SVINVDVMDLLTKTGLWDIQBELNKLTKTHYSPKPFDRGLGRLOGLKYVVRHFAFVYL 177
Db 136 SEEQARAVQMSKVLIOFLQKAKNLDAITTPTTNASLLTKLQANQWLQDMTHLIL 195
QY 178 SAMEXFAGQAVRVL 191
Db 196 RSFKEFLQSSLRAL 209

RESULT 8
Q9TTH3 PRELIMINARY; PRT; 209 AA.
AC Q9TTH3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-6 (Fragment).
GN Name=IL-6;
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes
RT in four species of owl monkey."
RL Immunogenetics 54:645-653(2002).
DR EMBL; AF097323; AAF21298.1; -.
DR HSSP; P05231; 1ALUJ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMFG.
DR ProDom; PD004356; Interleukin_6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
DR CARBOHYD; 172 172 N-linked (GlcNAc...) (Potential).
DR CARBOHYD; 172 172 N-linked (GlcNAc...) (Potential).
DR SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;

Query Match 16.6%; Score 182; DB 2; Length 209;
Best Local Similarity 26.5%; Pred. No. 1.5e-08;
Matches 41; Conservative 36; Mismatches 78; Indels 0; Gaps 0;

QY 37 QRLNWLWIDCFRDLCTVRTGICKGILEPAAIFHLKLPAINDTDHGILGFNETSCILKK 96
Db 55 KHIRVILEGISALRKEICDKSNWCSSKEALAEENLNLPKWAEGKCGFQSGFNEETCLVK 114
QY 97 LADGFFFEVLFKFLTTEFGKSVINVDVMDLLTKTGLWDIQBELNKLTKTHYSPKPFDRG 156
Db 115 IITGLLEFEVLYLQNRPESSKEAGAVQMSKGLQSLQKAKNLSAIAATPDATNAS 174
QY 157 LLGRLOGLKYVVRHFAFVYLSAMEKFAQAVRVL 191
Db 175 LLMKLQAOQWLQGVVTHILRSFKEFLQSSLRAL 209

RESULT 9
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```
IL6_MACMU
ID IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAC 2;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
DR EMBL; L26028; ARA99978.1; -.
DR HSSP; P05231; 1ALUJ.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMFG.
DR PRINTS; PR00434; INTERLEUKIN_6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 By similarity.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
DR SEQUENCE 212 AA; 23728 MW; 4130DFE0CF08CCAD CRC64;

Query Match 16.5%; Score 181; DB 1; Length 212;
Best Local Similarity 25.5%; Pred. No. 1.9e-08;
Matches 50; Conservative 40; Mismatches 98; Indels 8; Gaps 2;

QY 4 PKLNSLLVGSU----LVSGTRGKLPDAPEF-----KDLLIQRLNNWMLWVIDECPDLCY 55
Db 14 FSLGLLLVPAFAFPAPVLPDGEDSKNVAAPHSQPTTSERIDKHIRYILDGISALRKETCN 73
QY 56 RTGICKGILEPAAIFHLKLPAINDTDHGILGFNETSCIKKLADGFFFEVLFKFLTTEF 115
Db 74 RSNWCSSKEALAEENLNLPKWAEGKCGFQSGFNEETCLVKIITGLLEFEVLYLQNR 133
QY 116 GKSVINVDVMDLLTKTGLWDIQBELNKLTKTHYSPKPFDRGLGRLOGLKYVVRHFAF 175
Db 134 ESSEEQARAVQMSKVLIOFLQKAKNLDAITTPTTNASLLTKLQANQWLQDMTHL 193
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QY 176 VLSMEKEPAGQAVRVL 191
 Db 194 ILRSFKFQSLNRL 209

RESULT 10
 IL6_PIG
 ID IL6_PIG STANDARD; PRT; 212 AA.
 AC P26893; Q95KN6;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91338547; PubMed=1873476; DOI=10.1016/1043-4666(91)90494-X;
 RA Richards C., Saklatvala J.;
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
 expression of mRNA in synovial fibroblasts in vitro.";
 RL Cytokine 3:269-276(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92360284; PubMed=1497880;
 RA Mathialagan N., Bixby J.A., Roberts M.R.;
 RT "Expression of interleukin-6 in porcine, ovine, and bovine
 preimplantation conceptuses.";
 RL Mol. Reprod. Dev. 32:324-330(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Landrace x Meishan; TISSUE=Blood;
 RA Liu S., Meng M., Gao R.;
 RT "Cloning and expression of interleukin 6 gene from Landrace x Meishan
 hybrid swine.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 functions: it plays an essential role in the final differentiation
 of B-cells into Ig-secreting cells, it induces myeloma and
 plasmacytoma growth, it induces nerve cells differentiation, in
 hepatocytes it induces acute phase reactants.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: Belongs to the IL-6 superfamily.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M86722; AAC37333.1; -.
 CC EMBL; M80258; AAC27127.1; -.
 CC EMBL; AF309651; AAG27730.1; -.
 CC PIR; I46590; I46590.
 CC PIR; I46621; I46621.
 CC HSP; P05231; IALU.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR003573; IL6_MGF_GCSF.
 CC InterPro; IPR003574; Interleukin_6.
 CC Pfam; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSFMGF.
 CC PRINTS; PR00434; INTERLEUKIN6.
 CC ProDom; PD004356; Interleukin_6; 1.
 CC SMART; SM00126; IL6; 1.
 CC PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 By similarity.
 FT CHAIN 30 212 Interleukin-6.

FT DISULFID 72 78 By similarity.
 FT DISULFID 101 111 By similarity.
 FT CONFLICT 30 E -> G (in Ref. 1).
 SQ SEQUENCE 212 AA; 23952 MW; 1E736FB230B4FC5D CRC64;

Query Match 16.5%; Score 180.5; DB 1; Length 212;
 Best Local Similarity 23.9%; Pred. No. 2.1e-08;
 Matches 47; Conservative 46; Mismatches 87; Indels 17; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAPEPF-----KDLIIQLNLMWLVIDECPRDLCVRT 57
 Db 16 LGILLVWATFPTPERLEEDAKGDAVSQMLFTSPDKTEELIKYILKISAMRKEMCKY 75
 QY 58 GICKGILEPAAIFHLKLPAINDTDHCGILIGFNETSCLKLADGFEFEVLFKPLTTBFGK 117
 Db 76 EKCEKSEKVLAEENLNLPKMAEKDGCFCQSGFNQETCLMRTTGLVFEQIVLDYLQKEYS 135
 QY 118 SVINVDVMELLTKLGHWDIOEELNKLTKTHYSPPKPDRLGLRLQGLKYLKWRHPASPYVL 177
 Db 136 NKGNEVAQVISTKALIQTLRQKGNPKDKATTPNPTTNAAGLLDLQSQNEWMKNTKIIL 195
 QY 178 SAME---KPAQOAVRVL 191
 Db 196 RSLDFLQFSLRIRIM 212

RESULT 11
 QY7540 PRELIMINARY; PRT; 209 AA.
 ID QY7540 PRELIMINARY; PRT; 209 AA.
 AC QY7540;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 GN Name=IL-6;
 OS Aotus nancymae (Ma's night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
 RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Patarroyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey.";
 RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF014510; AAD01536.1; -.
 DR HSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT NON_TER 1 1
 FT NON_TER 209 209
 SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 16.3%; Score 179; DB 2; Length 209;
 Best Local Similarity 26.5%; Pred. No. 2.9e-08;
 Matches 41; Conservative 34; Mismatches 80; Indels 0; Gaps 0;

QY 37 QRLNWMWLVIDECPRDLCVRTGICKGILEPAAIFHLKLPAINDTDHGILIGFNETSCLKK 96
 Db 55 KHIRYILDGITSALRKETCNKSNKNCSSKEALAENLNLPRMAEKDGCFCQSGFNTECLVK 114


```
QY 97 LADGFEFVRLFKLTTRFGKSVINVDVWMLLTKTGLWDIOELNKLTKTHYSPKFDG 156
Db 115 IITGLLEFVYIYQNRFESEBQARVOMTKVLQFLQKAKNLDIAITPDPTTNAS 174
QY 157 LLGRQLGKYVVRHFASFVYLSAMEKFAQAVRVL 191
Db 175 LUTLQAQNWQLQDMTHLILASFKEFLQSSLRAL 209

RESULT 12
Q8MJ75 PRELIMINARY; PRT; 212 AA.
AC Q8MJ75;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IL-6.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee D., Yoo H., Choi I.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF518322; AM474938.1; -.
DR HSP; P05231; IALU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 212 AA; 23881 MW; 1F540E7030BCFD77 CRC64;

Query Match 16.2%; Score 177.5; DB 2; Length 212;
Best Local Similarity 23.9%; Pred. No. 48-08;
Matches 48; Conservative 48; Mismatches 80; Indels 25; Gaps 4;

QY 12 VGSLLVSGTR-----GKLPD-----APEFEKDLIIQRLNWLWVIDSCFRDL 53
Db 16 LGLLLVMATAFTPTGRLEDAKGDATSKMLFTSPDKTEEL-----IKYLKGISARREM 71
QY 54 CVRTGICGILPAAIFHLKLPAINDTDHCGLIGFNETSCLKLADGPFEPVLPKFLTT 113
Db 72 CEKYECENSKVLAENNLNLPMAEKDGCQFSGFNQETCLMRITTLGLVFEQIYLDLYLQK 131
QY 114 EFGKSVINVDVWMLLTKTGLWDIOELNKLTKTHYSPKFDGILGRLOGLKYVVRHFAS 173
Db 132 EYESKNGVNEAVOISTKALIQTLRQKGNPKATTNPPTNAGLLDKLQSQNEWMKNTKI 191
QY 174 FYVLGSAE---KFAGQAVRVL 191
Db 192 IILRSLEDPLQFSLRATRIM 212

RESULT 13
IL6_HORSE
ID IL6_HORSE STANDARD; PRT; 208 AA.
AC Q95T81; O19007; O46568;
DT 01-NOV-1997 (rel. 35, Created)
DT 15-JUL-1999 (rel. 38, Last sequence update)
DT 05-JUL-2004 (rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
```

```
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Swiderski C.E., Sobol G., Lunn D.P., Horchov D.W.;
RL Molecular cloning, sequencing, and expression of equine interleukin-6.;
RL Vet. Immunol. Immunopathol. 77:213-220(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RL "Molecular cloning of equine interleukin-6.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RL "Cloning and expression of equine interleukin-6.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC
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CC
CC EMBL; U64794; AAB87703.1; -.
CC EMBL; AF005227; AAB62246.1; -.
CC EMBL; AF041975; AAC04574.1; -.
CC PIR; T09216; T09216.
CC HSP; P05231; IALU.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR003573; IL6_MGF_GCSF.
CC InterPro; IPR003574; Interleukin_6.
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6GCSFMGF.
CC PRODOM; PD004356; Interleukin_6; 1.
CC SMART; SM00126; IL6; 1.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 208 Interleukin-6.
FT DISULFD 69 75 By similarity.
FT DISULFD 98 108 By similarity.
FT CARBOHYD 71 71 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 184 184 N-linked (GLCNAC. .) (Potential).
FT CONFLICT 4 5 LS -> FF (in Ref. 1).
FT CONFLICT 8 8 T -> A (in Ref. 3).
FT CONFLICT 137 137 I -> V (in Ref. 2).
FT CONFLICT 205 205 V -> I (in Ref. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 15.8%; Score 173.5; DB 1; Length 208;
Best Local Similarity 26.0%; Pred. No. 9.1e-08;
Matches 51; Conservative 37; Mismatches 89; Indels 19; Gaps 5;

QY 12 VGSLLVSGTRKLP-----DAPEFEKDLII-----QRLNWLWVIDSCFRDLCYRTGIC 60
Db 16 LGLLLVMATAFTPTPLPGLGEDETTSGNPLLTADTKQHKIQLKISALKNEMCNFSGK 75
QY 61 KGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKLADGPFEPVLPKFLTTTEFGKSVI 120
```


Db 76 ENSKEVLAENNLNPKWAEDKCGQSGFNOSTLKMKTITGLSEFQIYLVLEQNEFKGEKE 135
 Qy 121 NVDVWELLTKTGLWDIOBELNKLTKTHYS--PPKFRDGLRLQGLKLVYVRHFAFVYVLS 178
 Db 136 NIKTMQISTKVL---VQILQKMKNPVPTTDPDTAKSSLLAKLHNSQEWLNKNTTHILIR 192
 Qy 179 AME---KPAQOAVRVL 191
 Db 193 SLEDFLOFSLRAVRIM 208

RESULT 14
 IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94162386; PubMed=8117820;
 RA Ohashi T., Matsumoto Y., Watari T., Goitsuka R., Tsujimoto H.,
 RA Hasegawa A.;
 RT "Molecular cloning of feline interleukin-6 cDNA."
 RL J. Vet. Med. Sci. 55:941-944 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=94052249; PubMed=8234373;
 RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
 RT "Molecular cloning and characterization of a cDNA encoding feline
 interleukin-6";
 RL Proc. Soc. Exp. Biol. Med. 204:301-305 (1993).
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 CC -----
 CC EMBL; L16914; AAA16620.1; -;
 CC EMBL; D13227; BAA02507.1; -;
 CC PIR; I46084; I46084.
 CC HSP; P05231; IL6.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR003573; IL6_MGF_GCSP.
 CC InterPro; IPR003574; Interleukin_6.
 CC Pfam; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSPMGF.
 CC PRINTS; PR00434; INTERLEUKIN_6.
 CC SMART; SM00126; IL6; 1.
 CC PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 27 Potential.
 FT CHAIN 28 208 Interleukin-6.
 FT DISULFID 68 74 By similarity.

FT DISULFID 97 107 By similarity.
 FT CONFLICT 2 2 T -> N (in Ref. 2).
 FT CONFLICT 45 45 S -> P (in Ref. 2).
 FT CONFLICT 133 133 E -> K (in Ref. 2).
 FT CONFLICT 173 187 AKLQSEEWLRHTTI -> LSCSHRRVAAEHNH (in
 Ref. 2).
 FT CONFLICT 200 201 FS -> LR (in Ref. 2).
 SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;
 Query Match 14.9%; Score 163.5; DB 1; Length 208;
 Best Local Similarity 26.8%; Pred. No. 7.5e-07;
 Matches 55; Conservative 39; Mismatches 84; Indels 27; Gaps 7;
 Qy 4 FKLWLLLV-----GSLVSGTRGKLPDAPFEKDLIQLRLNMLWVDECFRDLCYR 56
 Db 14 FSLGLLVVATAFPTPLGGDATSNRLPUT---SADKMEELIKYILGKISALKKEMCDN 70
 Qy 57 TGICKGILEPAAIFHLKLPAINDTDCGLIGFNETSCLKLADGFFPEFVFLFELTTEP- 115
 Db 71 YNKCEDSKAALNNLNLKLAEGKCGFQSGFNQETCLTRITTTGLQBFQIYLFQDKYE 130
 Qy 116 ----GKSV-INVDVMEELTKTGLWDIOBELNKLTKTHYSPPKFRDGLRLQGLKLVYVR 169
 Db 131 GDEENAKSVTSTNVLLQMLKRGKKN-QDEV-----IPVPTVEVGLQKQSQEWEWR 183
 Qy 170 HFASFVYVLSAME---KPAQOAVRVL 191
 Db 184 HTTILTLRLREDFLOFSLRAVRIM 208

RESULT 15
 IL6_LAMGL STANDARD; PRT; 211 AA.
 AC Q865X6;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Name=IL6;
 OS Lama glama (Llama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Raadan O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
 RA Onuma M.;
 RT "Cloning and sequence analysis of cytokine cDNAs of llama and camel."
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC -----
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 CC -----
 CC EMBL; AB107647; BAC75384.1; -;
 CC HSP; P05231; IL6.
 CC InterPro; IPR009079; 4 helix cytokine.
 CC InterPro; IPR003573; IL6_MGF_GCSP.
 CC InterPro; IPR003574; Interleukin_6.
 CC Pfam; PF00489; IL6; 1.
 CC PRINTS; PR00433; IL6GCSPMGF.
 CC PRINTS; PR00434; INTERLEUKIN_6.

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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:09:54 ; Search time 21.0448 Seconds
(without alignments)
349.180 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKXLDGFFFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	19	2 AAW23945	Aaw23945 Human her
2	103	100.0	185	2 AAW95015	Aaw95015 Kaposi's
3	103	100.0	204	2 AAW40103	Aaw40103 Human her
4	103	100.0	204	2 AAW23944	Aaw23944 Human her
5	103	100.0	204	2 AAW74570	Aaw74570 Kaposi sa
6	61	59.2	118	7 ADH76487	Adh76487 Interleuk
7	61	59.2	125	7 ADH76486	Adh76486 Interleuk
8	61	59.2	148	4 AAU02910	Aau02910 Angiotens
9	61	59.2	157	7 ADF17513	Adf17513 MB-2 amin
10	61	59.2	162	2 AAR77391	Aar77391 Human mut
11	61	59.2	162	2 AAW00131	Aaw00131 Human int
12	61	59.2	163	2 AAW00132	Aaw00132 Human int
13	61	59.2	166	6 ABU62834	Abu62834 Human int
14	61	59.2	166	6 ABU62837	Abu62837 Monkey in
15	61	59.2	166	7 ADC20004	Adc20004 Rhesus mo
16	61	59.2	166	7 ADC20001	Adc20001 Human int
17	61	59.2	167	7 ADF17512	Adf17512 MB-1 amin
18	61	59.2	167	2 AAR77649	Aar77649 Human int
19	61	59.2	169	2 AAR77387	Aar77387 Human IL-
20	61	59.2	174	2 AAR75342	Aar75342 Hybrid hu
21	61	59.2	176	2 AAR75341	Aar75341 Hybrid hu
22	61	59.2	177	2 AAR77388	Aar77388 Human IL-
23	61	59.2	179	2 AAR75334	Aar75334 Human int
24	61	59.2	182	6 ABP72700	Abp72700 Human int
25	61	59.2	183	2 AAR60125	Aar60125 Human int

ALIGNMENTS

RESULT 1

AAW23945
ID AAW23945 standard; protein; 19 AA.
AC AAW23945;
XX
DT 01-JUL-1998 (first entry)
DE Human herpesvirus 8 interleukin-6 fragment.
XX
XX interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
KW Antibodies; diagnosis; treatment.
XX
OS Human herpesvirus 8.
XX
PN WO9803657-A1.
XX
PD 29-JAN-1998.
XX
PF 19-JUL-1996; 96WO-EP003199.
XX
PR 19-JUL-1996; 96WO-EP003199.
XX
PA (BEHW) BEHRING DIAGNOSTICS GMBH.
PA (UYN) UNIV NEW YORK STATE.
PI Fleckenstein B, Albrecht J, Neipel F, Friedman-Kien A, Huang Y;
XX
DR WPI; 1998-120781/11.
XX
PT Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA
PT - and related nucleic acid and antibodies, used for diagnosis and
PT treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
XX
XX Claim 4; Page 8; 19pp; English.
PS
XX
CC The interleukin-6 (IL-6) fragment and protein AAW23944 can be used to
CC detect antibodies and antibodies can be used to detect IL-6. This can be
CC used for the diagnosis of HHV8 infection or associated diseases such as
CC Kaposi sarcoma or kidney cell carcinoma. Antibodies, proteins and the
CC gene sequence can all be used in the treatment of infections and diseases
CC as mentioned above
XX
SQ Sequence 19 AA;

Query Match 100.0%; Score 103; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 GFNETSCLKKLADGFFFEF 19
DB      1 GFNETSCLKKLADGFFFEF 19

RESULT 2
AAW95015
ID      AAW95015 standard; peptide; 185 AA.
AC      AAW95015;
XX      27-AUG-2003 (revised)
DT      21-MAY-1999 (first entry)
XX      Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.
DE      Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;
KW      inflammatory condition; drug screening; human; IL-6.
XX      Human herpesvirus 8.
OS      WO9905280-A1.
PN      04-FEB-1999.
XX      24-JUL-1998; 98WO-US015423.
PF      25-JUL-1997; 97US-00900905.
PR      (SCHE ) SCHERING CORP.
XX      Bazan JF;
PI      WPI; 1999-142935/12.
XX      Newly isolated or recombinant polynucleotide encoding mammalian cytokine
PT      interleukin-B30 (IL-B30), including fragments - useful for regulating
PT      activation, development, differentiation and function of various cell
PT      types, and for diagnosing and treating conditions associated with IL-B30.
XX      Disclosure; Page 11-12; 83pp; English.
PS      This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
XX      polypeptides. Host cells containing a vector comprising the IL-B30
CC      nucleic acids are used for the recombinant production of the proteins.
CC      The polynucleotides are useful for diagnosis of IL-B30 mediated
CC      conditions, and forensic science (e.g. to distinguish rodent from human,
CC      or as a marker to distinguish between different cells exhibiting
CC      differential expression or modification patterns). The IL-B30 (including
CC      fragments), together with antibodies that bind to IL-B30 are useful for
CC      teaching purposes. They are also used for treating conditions associated
CC      with abnormal physiology or development, including inflammatory
CC      conditions. The polypeptide cytokine should mediate cytokine synthesis
CC      and proliferation in cells. IL-B30 is useful for drug screening to
CC      identify compounds having binding affinity to IL-B30. The present
CC      sequence represents a Kaposi's sarcoma herpes virus IL-6. (Updated on 27
CC      -AUG-2003 to correct OS field.)
XX      Sequence 185 AA;
SQ      Query Match      100.0%; Score 103; DB 2; Length 185;
          Best Local Similarity 100.0%; Pred. No. 1.7e-08;
          Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFNETSCLKKLADGFFFEF 19
DB      68 GFNETSCLKKLADGFFFEF 86

RESULT 3
AAW40103
ID      AAW40103 standard; protein; 204 AA.

```

```

XX      AAW40103;
AC      27-AUG-2003 (revised)
XX      15-JUL-1998 (first entry)
DT      Human herpesvirus 8 (HHV-8) interleukin-6.
DE      DL-B; thymidylate synthase; dihydrofolate reductase; primer; HHV-8;
KW      Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;
KW      Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; vIL-6.
XX      Human herpesvirus 8.
OS      WO9804284-A1.
PN      05-FEB-1998.
XX      24-JUL-1997; 97WO-US012931.
PF      25-JUL-1996; 96US-0022591P.
PR      (UYJO ) UNIV JOHNS HOPKINS.
XX      Hayward GS, Nicholas J, Reitz MR, Hardwick JM;
PI      WPI; 1998-130422/12.
XX      New human herpes virus gene region containing 8 open reading frames -
PT      useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based large
PT      cell lymphoma.
XX      Claim 1; Page 59-60; 84pp; English.
PS      The sequence represents a novel human herpesvirus 8 (HHV-8) interleukin-
XX      6. The invention claims for novel genes, which includes the viral
CC      interleukin-6 gene, found at the divergent DL-B locus. HHV-8 divergent
CC      locus DL-B lies between open reading frames 11 and 17. Sequencing of the
CC      HHV-8 divergent locus DL-B revealed the presence of nine viral ORFs with
CC      gene products related to cellular proteins. These proteins include the
CC      thymidylate synthase (TS, AAW40100), dihydrofolate reductase (DHFR, see
CC      AAW40101), Bcl-2 homologue (AAW40102), IE-1A (AAW40107), IE-1B (AAW40108)
CC      and four cytokines which include viral interleukin-6 (vIL-6), viral
CC      macrophage inhibitory protein (vMIP)-1A (AAW40104) and -1B (AAW40105) and
CC      beta-chemokine-like (BCK, AAW40106) protein. The invention claims the
CC      mentioned proteins and a polynucleotide containing HHV-8 genes encoding
CC      one or more of these proteins. The invention also claims that the
CC      polynucleotide and the proteins may be used directly or indirectly, e.g.
CC      using antibodies to the proteins to diagnose an HHV-8 associated
CC      disease, e.g. Kaposi's sarcoma, Castleman's disease, multiple myeloma and
CC      body cavity based large cell lymphoma (BCBL). The proteins have also been
CC      claimed to be useful in screening compounds for drugs to treat HHV-8
CC      diseases. (Updated on 27-AUG-2003 to correct OS field.)
XX      Sequence 204 AA;
SQ      Query Match      100.0%; Score 103; DB 2; Length 204;
          Best Local Similarity 100.0%; Pred. No. 1.9e-08;
          Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GFNETSCLKKLADGFFFEF 19
DB      87 GFNETSCLKKLADGFFFEF 105

RESULT 4
AAW23944
ID      AAW23944 standard; protein; 204 AA.
XX      AAW23944;
AC      30-JUN-1998 (first entry)
DT
XX

```

DE Human herpesvirus 8 interleukin-6.
 XX interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
 KW antibody; diagnosis; treatment.
 XX
 OS Human herpesvirus 8.
 XX
 PN WO9803657-A1.
 XX
 XX 29-JAN-1998.
 XX
 XX 19-JUL-1996; 96WO-EP003199.
 XX
 XX 19-JUL-1996; 96WO-EP003199.
 XX
 XX (BEHW) BEHRING DIAGNOSTICS GMBH.
 PA (UJNY) UNIV NEW YORK STATE.
 XX
 XX Fleckenstein B, Albrecht J, Neipel F, Friedman-Kien A, Huang Y;
 PI WPI; 1998-120781/11.
 XX
 XX Viral interleukin-6 produced recombinantly from human herpes virus 8 DNA
 PT - and related nucleic acid and antibodies, used for diagnosis and
 PT treatment of herpes 8 infection or related diseases, e.g. Kaposi sarcoma.
 XX
 XX Claim 2; Fig 2; 19pp; English.
 XX PS
 XX The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence
 CC can be used to detect antibodies and antibodies can be used to detect IL-
 CC 6. This can be used for the diagnosis of HHV8 infection or associated
 CC diseases such as Kaposi sarcoma or kidney cell carcinoma. Antibodies,
 CC proteins and the gene sequence can all be used in the treatment of
 CC infections and diseases as mentioned above
 XX
 XX Sequence 204 AA;
 *SQ
 Query Match 100.0%; Score 103; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 87 GFNETSCLKKLADGFFFE 105
 RESULT 5
 AAW74570
 ID AAW74570 standard; protein; 204 AA.
 XX
 AC AAW74570;
 XX
 XX 04-DEC-1998 (first entry)
 DT
 XX Kaposi sarcoma herpes-like virus/interleukin-6.
 DE
 XX Kaposi sarcoma herpes-like virus/interleukin-6; PCR; primer;
 KW antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis;
 KW monoclonal gammopathy of undetermined significance; MGUS; malignant;
 KW interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma;
 KW systemic lupus erythematosus; amplification.
 XX
 OS Synthetic.
 XX
 XX WO9835684-A2.
 PN
 XX 20-AUG-1998.
 PD
 XX 12-FEB-1998; 98WO-US002820.
 PF
 XX 14-FEB-1997; 97US-00800710.
 PR
 PR 11-NOV-1997; 97US-00967504.
 XX

PA (BERE/) BERENSON J R.
 PA (RETT/) RETTIG M B.
 PA (VESC/) VESCIO R A.
 XX
 PI Berenson JR, Rettig MB, Vescio RA;
 XX WPI; 1998-480765/41.
 DR N-PSDB; AAV54070.
 DR
 XX Treatment of multiple myeloma and monoclonal myopathy with antiviral
 PT agent - active against Kaposi sarcoma virus, or with inhibitory nucleic
 PT acid or antibody against this virus.
 XX
 XX Disclosure; Fig 5B; 137pp; English.
 XX
 XX This is the amino acid sequence of the Kaposi sarcoma herpes-like
 CC virus/interleukin-6, used in the method of the invention. In this method,
 CC an antiviral agent effective against Kaposi sarcoma herpes-like virus
 CC (KSHV), is used to prevent progression of MGUS to multiple myeloma or
 CC related malignancy. KHSV- and/or interleukin-6 related disorders such as
 CC specifically Alzheimer's disease, multiple sclerosis, rheumatoid
 CC arthritis, systemic lupus erythematosus, scleroderma and malignancies of
 CC kidney or head/neck. The vaccines (comprising a KHSV-specific immunogen)
 CC is used to produce a therapeutic and/or prophylactic response
 XX
 XX Sequence 204 AA;
 SQ
 Query Match 100.0%; Score 103; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 87 GFNETSCLKKLADGFFFE 105
 RESULT 6
 ADH76487
 ID ADH76487 standard; protein; 118 AA.
 XX
 AC ADH76487;
 XX
 XX 22-APR-2004 (first entry)
 DT
 XX Interleukin-6 inhibiting human PAC3 protein, SEQ ID No 4.
 DE
 XX PAC3; interleukin-6; IL-6; inhibitor; IL-6-inhibitory; lymphoma;
 KW leukaemia; myeloma; carcinoma; sarcoma; chronic inflammation; bacterial;
 KW viral infection; osteolysis; degenerative disease;
 KW immunological disorder; transgenic animal; human.
 XX
 OS Homo sapiens.
 XX
 XX FR2833011-A1.
 PN
 XX 06-JUN-2003.
 PD
 XX 04-DEC-2001; 2001FR-00015623.
 PF
 XX 04-DEC-2001; 2001FR-00015623.
 PR
 XX (UJLY-) UNIV LYON 1 BERNARD CLAUDE.
 PA (BERA-) CENT BERARD LEON.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PA (HOSP-) HOSPICES CIVILS LYON.
 XX
 XX Blay JY, Alberti L;
 PI
 XX WPI; 2003-471810/45.
 DR
 XX New protein PAC3, useful for treating cancers, is an inhibitor of
 PT interleukin-6, also related peptides, nucleic acid, antisense
 PT oligonucleotides and transformed cells.
 PT

XX PS Claim 3; SEQ ID NO 4; 39pp; French.

XX CC The invention relates to a novel protein, PAC3, which inhibits

XX CC interleukin-6 (IL-6) and has a 125 amino acid sequence, given in the

XX CC specification. The invention further relates to: peptide fragments of

XX CC PAC3 with IL-6-inhibitory activity, formed by addition, suppression

XX CC and/or replacement of one or more amino acids; a nucleic acid that

XX CC encodes PAC3 or the fragments of the nucleic acid; antisense

XX CC oligonucleotides that block transcription or translation of PAC3 or its

XX CC fragments, able to hybridize to the PAC3 coding nucleic acid; a

XX CC transgenic, non-human animal that expresses a transgene for PAC3 or its

XX CC fragments; an expression vector containing PAC3 coding nucleic acid and

XX CC expression elements; and microorganisms or host cells transformed with

XX CC the vector containing the PAC3 coding nucleic acid and expression

XX CC elements. The PAC3 protein, and its active fragments, are used to treat

XX CC lymphoma, leukaemia, myeloma, carcinoma and sarcoma, other conditions

XX CC chronic inflammation, bacterial or viral infections, osteolysis in

XX CC degenerative diseases and immunological disorders. The nucleic acid that

XX CC encodes PAC3 can be used for recombinant production of the protein and to

XX CC prepare transgenic animals, useful as models for studying, in vivo,

XX CC perturbations of the cell cycle and proliferation caused by abnormal or

XX CC excessive expression of the PAC3 coding nucleic acid, or its truncated or

XX CC mutated forms. This sequence represents a human PAC3 protein of the

XX CC invention.

XX SQ Sequence 118 AA;

Query Match 59.2%; Score 61; DB 7; Length 118;
Best Local Similarity 57.9%; Pred. No. 0.076; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 2;

QY 1 GFNETSCLKLADGPFPE 19
||||:|:|:|
Db 11 GFNETCLVKIITGLLEFE 29

RESULT 7
ADH76486
ID ADH76486 standard; protein; 125 AA.
AC ADH76486;
DT 22-APR-2004 (first entry)
DE Interleukin-6 inhibiting human PAC3 protein, SEQ ID No 3.
KW PAC3; interleukin-6; IL-6; inhibitor; IL-6-inhibitory; lymphoma;
KW leukaemia; myeloma; carcinoma; sarcoma; chronic inflammation; bacterial;
KW viral infection; osteolysis; degenerative disease;
KW immunological disorder; transgenic animal; human.
XX Homo sapiens.
XX FR2833011-A1.
XX 06-JUN-2003.
XX 04-DEC-2001; 2001PR-00015623.
XX 04-DEC-2001; 2001PR-00015623.
XX (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
XX (BERA-) CENT BERARD LEON.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX (HOSP-) HOSPICES CIVILS LYON.
XX Blay JY, Alberti L;
XX WPI; 2003-471810/45.
XX New protein PAC3, useful for treating cancers, is an inhibitor of

PT interleukin-6, also related peptides, nucleic acid, antisense
PT oligonucleotides and transformed cells.

XX PS Claim 1; SEQ ID NO 3; 39pp; French.

XX CC The invention relates to a novel protein, PAC3, which inhibits

XX CC interleukin-6 (IL-6) and has a 125 amino acid sequence, given in the

XX CC specification. The invention further relates to: peptide fragments of

XX CC PAC3 with IL-6-inhibitory activity, formed by addition, suppression

XX CC and/or replacement of one or more amino acids; a nucleic acid that

XX CC encodes PAC3 or the fragments of the nucleic acid; antisense

XX CC oligonucleotides that block transcription or translation of PAC3 or its

XX CC fragments, able to hybridize to the PAC3 coding nucleic acid; a

XX CC transgenic, non-human animal that expresses a transgene for PAC3 or its

XX CC fragments; an expression vector containing PAC3 coding nucleic acid and

XX CC expression elements; and microorganisms or host cells transformed with

XX CC the vector containing the PAC3 coding nucleic acid and expression

XX CC elements. The PAC3 protein, and its active fragments, are used to treat

XX CC lymphoma, leukaemia, myeloma, carcinoma and sarcoma, other conditions

XX CC chronic inflammation, bacterial or viral infections, osteolysis in

XX CC degenerative diseases and immunological disorders. The nucleic acid that

XX CC encodes PAC3 can be used for recombinant production of the protein and to

XX CC prepare transgenic animals, useful as models for studying, in vivo,

XX CC perturbations of the cell cycle and proliferation caused by abnormal or

XX CC excessive expression of the PAC3 coding nucleic acid, or its truncated or

XX CC mutated forms. This sequence represents a human PAC3 protein of the

XX CC invention.

XX SQ Sequence 125 AA;

Query Match 59.2%; Score 61; DB 7; Length 125;
Best Local Similarity 57.9%; Pred. No. 0.08; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 2;

QY 1 GFNETSCLKLADGPFPE 19
||||:|:|:|
Db 11 GFNETCLVKIITGLLEFE 29

RESULT 8
AAU02910
ID AAU02910 standard; protein; 148 AA.
AC AAU02910;
DT 12-SEP-2001 (first entry)
DE Angiotensin converting enzyme (ACEV) splice variant protein #10.
KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.
XX Homo sapiens.
XX WO200136632-A2.
XX 25-MAY-2001.
XX 17-NOV-2000; 2000WO-IL000766.
XX 17-NOV-1999; 99IL-00132978.
XX 10-DEC-1999; 99IL-00133455.
XX (COMP-) COMPUGEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
 XX WPI; 2001-336004/35.
 DR N-PSDB; AAS06010.
 XX Novel alternative splicing variants e.g. variant of angiotensin
 PT converting enzyme (ACEV), useful in identifying candidate compounds
 PT capable of binding to the variant and to detect anti-variant antibodies.
 XX Claim 4; Fig 10; 519pp; English.
 PS
 XX The sequence represents an angiotensin converting enzyme splice variant
 CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis
 XX SQ Sequence 148 AA;
 Query Match 59.2%; Score 61; DB 4; Length 148;
 Best Local Similarity 57.9%; Pred. No. 0.095;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 *QY 1 GFNETSCLKXKLADGFFFE 19
 Db 41 GFNEETCLVKIITGLLEFE 59
 |||||:|:|:|
 RESULT 9
 ADF17513
 ID ADF17513 standard; protein; 157 AA.
 XX AC ADF17513;
 XX 12-FEB-2004 (first entry)
 XX MB-2 amino acid sequence.
 XX protein structure analysis; genetic analysis.
 XX Synthetic.
 XX WO2003091720-A1.
 XX 06-NOV-2003.
 XX 25-APR-2003; 2003WO-JP005344.
 XX 26-APR-2002; 2002JP-00127399.
 XX (AJIN) AJINOMOTO CO INC.
 XX (UMEY) UMEYAMA H.
 XX Umeyama H, Yamada N, Suzuki E, Hirayama K;
 XX WPI; 2003-877362/81.
 XX Protein structure analysis comprising measuring a fragmented spectrum,
 PT determining classification information, determining information about an
 PT easily cut off region, estimating the stereostructure of the protein and
 PT outputting results.

XX Example 5; Fig 18; 103pp; Japanese.
 PS
 XX The present invention describes a protein structure analysis method
 CC comprising measuring a fragmented spectrum by dividing the target protein
 CC into several segments, determining the classification information of the
 CC segmented ion corresponding to the amino acid sequence based on the
 CC spectrum, determining an easily cut off region based on the
 CC classification based on the segmented location, estimating the stereo
 CC structure of the protein, and outputting result of estimation data and
 CC easy cut off region information. Also described: (1) a similar method
 CC wherein before estimating the stereo structure, residual solvent
 CC information is determined based on the locations where the amino acid is
 CC in contact with a solvent and on the spectrum and classification
 CC information; (2) a similar method wherein a composite of a protein and a
 CC compound is fragmented, and before estimating the stereo structure the
 CC interface information of mutual effect of the protein and/or compound is
 CC determined; (3) apparatus for carrying out the above methods; and (4)
 CC programs for carrying out the methods. The method can be used for genetic
 CC analysis. The present sequence represents an MB-2 amino acid sequence,
 XX which is used in an example from the present invention.
 XX SQ Sequence 157 AA;
 Query Match 59.2%; Score 61; DB 7; Length 157;
 Best Local Similarity 57.9%; Pred. No. 0.1;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKXKLADGFFFE 19
 Db 50 GFNEETCLVKIITGLLEFE 68
 |||||:|:|:|
 RESULT 10
 AAR77391
 ID AAR77391 standard; protein; 162 AA.
 XX AC AAR77391;
 XX 17-APR-1996 (first entry)
 XX Human mutant IL-6a'Cl (amino acids 5-19 and 44-50 deleted).
 DE Human interleukin-6; IL-6a'Cl mutant; increased stability; recombinant;
 XX production; deletion mutant; amino acids 5-19 and 44-50.
 XX Homo sapiens.
 OS JP07224097-A.
 XX 22-AUG-1995.
 XX 08-FEB-1994; 94JP-00014461.
 XX 08-FEB-1994; 94JP-00014461.
 XX (ASAG) ASAHI GLASS CO LTD.
 XX WPI; 1995-325556/42.
 DR N-PSDB; AAQ94346.
 XX Interleukin-6 mutant, related DNA and expression vectors - has higher
 PT stability than natural interleukin-6.
 XX Claim 1; Page 14; 18pp; Japanese.
 XX AAQ94346 encodes AAR77391 the human IL-6 deletion mutant IL-6a'Cl, which
 CC lacks the amino acids Gly5-Leu19 and Cys44-Cys50 of the wild type
 CC protein. The cDNA can be used for the recombinant prodn. of IL-6a'Cl,
 CC which has increased stability compared to wild type IL-6
 XX Sequence 162 AA;
 SQ

```
Query Match          59.2%; Score 61; DB 2; Length 162;
Best Local Similarity 57.9%; Pred. No. 0.1;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 55 GFNEETCLVKIITGLLEFE 73

RESULT 11
AAW00131
ID AAW00131 standard; protein; 162 AA.
XX
AC AAW00131;
XX
DT 09-APR-1997 (first entry)
XX
DE Human interleukin-6 fragment.
XX
KW Secretory; signal peptide; P-factor; multicloning vector; PCR;
KW animal protein; expression; production; recombinant; primer;
KW fission yeast; human; serum albumin; interleukin-6;
KW polymerase chain reaction; Schizosaccharomyces pombe; PO fragment.
XX
OS Homo sapiens.
XX
PN WO9623890-A1.
XX
PD 08-AUG-1996.
XX
PF 01-FEB-1996; 96WO-JP000198.
XX
PR 03-FEB-1995; 95JP-00017167.
XX
PA (ASAG ) ASahi GLASS CO LTD.
XX
PI Hama Y, Tohda H, Tsukamoto H, Nikaido K, Kumagai H;
XX
WPI; 1996-371438/37.
XX
PT Schizosaccharomyces pombe secretory signal peptide (P-factor) gene - for
PT production of vectors for expression of animal proteins in a fission
PT yeast, pref. S. pombe, host.
XX
PS Example 4; Page 28-29; 50pp; Japanese.
XX
CC A multicloning vector, comprising the human interleukin-6 (hIL-6) cDNA, a
CC Schizosaccharomyces pombe secretory signal peptide fragment or P-factor
CC fragment (PO fragment) DNA and preferably an animal cell viral promoter
CC sequence and a neomycin resistance gene, can be used for the efficient
CC production of a hIL-6 fragment, i.e. the present sequence, in a fission
CC yeast host, preferably S. pombe, culture
XX
SQ Sequence 162 AA;

Query Match          59.2%; Score 61; DB 2; Length 162;
Best Local Similarity 57.9%; Pred. No. 0.1;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 55 GFNEETCLVKIITGLLEFE 74

RESULT 13
ABU62834
ID ABU62834 standard; protein; 166 AA.
XX
AC ABU62834;
XX
DT 16-SEP-2003 (first entry)
XX
DE Human interleukin-6, IL-6.
XX
KW Human; interleukin-6; IL-6; cytokine; bone homeostasis; Paget's; disease;
KW multiple myeloma; post-menopausal bone loss.
XX
OS Homo sapiens.
XX
PN US2003068300-A1.
XX
PD 10-APR-2003.
XX
PF 19-SEP-2002; 2002US-00246946.
XX
PR 16-AUG-1996; 96US-0024115P.
XX
PR 29-APR-1997; 97US-00841035.
XX
PR 07-FEB-2000; 2000US-00499148.
XX
PA (AMHP ) WYETH.
XX
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PI Somers WS, Stahl ML, Seehra JS, Xu G, McDonagh TE, Yu H, Hong J;
 XX WPI; 2003-540877/51.
 XX
 XX Computer system useful for identifying agonist or antagonist of
 PT interleukin 6 activity or binding, comprises computer hardware and model
 PT of interleukin 6 structure.
 XX
 XX Disclosure; Fig 12; 37pp; English.
 PS
 XX The invention relates to a computer system comprising computer hardware
 CC and model of interleukin (IL)-6 structure, where the model has data set
 CC representing phasing statistics for the native crystal, root mean square
 CC (RMS) deviations from experimental distance restraints (Angstrom), RMS
 CC deviations from idealised covalent geometry, energetics, interhelical and
 CC kink angles and interhelical distances, residues conserved among 9
 CC species of IL-6, as given in specification. Also included are identifying
 CC a species which is an agonist or antagonist of IL-6 activity or binding
 CC using the computer system, an agonist or antagonist species identified by
 CC above mentioned method and identifying a substance that inhibits or
 CC mimics IL-6 activity or binding, using the computer system. IL-6 is a
 CC cytokine involved in bone homeostasis. Increased levels of IL-6 have been
 CC correlated with Paget's disease and multiple myeloma. IL-6 is also
 CC thought to be involved in post-menopausal bone loss. The present sequence
 CC is human IL-6
 XX
 XX Sequence 166 AA;
 SQ
 Query Match 59.2%; Score 61; DB 6; Length 166;
 Best Local Similarity 57.9%; Pred. No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 59 GFNEETCLVKIITGLLEFE 77
 RESULT 14
 ABU62837
 ID ABU62837 standard; protein; 166 AA.
 XX
 AC ABU62837;
 XX
 XX 16-SEP-2003 (first entry)
 DT
 XX Monkey interleukin-6, IL-6.
 DE
 XX Interleukin-6; IL-6; cytokine; bone homeostasis; Paget's; disease;
 KW multiple myeloma; post-menopausal bone loss; monkey.
 XX
 OS Macaca mulatta.
 XX
 XX US2003068300-A1.
 PN
 XX 10-APR-2003.
 PD
 XX
 XX 19-SEP-2002; 2002US-00246946.
 PF
 XX
 XX 16-AUG-1996; 96US-0024115P.
 PR
 XX 29-APR-1997; 97US-00841035.
 PR
 XX 07-FEB-2000; 2000US-00499148.
 XX
 XX (AMHP) WYETH.
 PA
 XX
 XX Somers WS, Stahl ML, Seehra JS, Xu G, McDonagh TE, Yu H, Hong J;
 PI WPI; 2003-540877/51.
 DR
 XX Computer system useful for identifying agonist or antagonist of
 PT interleukin 6 activity or binding, comprises computer hardware and model
 PT of interleukin 6 structure.
 XX
 XX Disclosure; Fig 12; 37pp; English.

XX The invention relates to a computer system comprising computer hardware
 CC and model of interleukin (IL)-6 structure, where the model has data set
 CC representing phasing statistics for the native crystal, root mean square
 CC (RMS) deviations from experimental distance restraints (Angstrom), RMS
 CC deviations from idealised covalent geometry, energetics, interhelical and
 CC kink angles and interhelical distances, residues conserved among 9
 CC species of IL-6, as given in specification. Also included are identifying
 CC a species which is an agonist or antagonist of IL-6 activity or binding
 CC using the computer system, an agonist or antagonist species identified by
 CC above mentioned method and identifying a substance that inhibits or
 CC mimics IL-6 activity or binding, using the computer system. IL-6 is a
 CC cytokine involved in bone homeostasis. Increased levels of IL-6 have been
 CC correlated with Paget's disease and multiple myeloma. IL-6 is also
 CC thought to be involved in post-menopausal bone loss. The present sequence
 CC is an IL-6 protein from a species other than human, used in the
 CC determination of the structure of human IL-6
 XX
 XX Sequence 166 AA;
 SQ
 Query Match 59.2%; Score 61; DB 6; Length 166;
 Best Local Similarity 57.9%; Pred. No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 59 GFNEETCLVKIITGLLEFE 77
 RESULT 15
 ADC20004
 ID ADC20004 standard; protein; 166 AA.
 XX
 AC ADC20004;
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX Rhesus monkey interleukin-6, IL-6.
 DE
 XX rhesus monkey; crystal; interleukin-6; IL-6;
 KW IL-6/IL-6 receptor interaction.
 XX
 OS Macaca mulatta.
 XX
 XX US6461604-B1.
 PN
 XX
 XX 08-OCT-2002.
 PD
 XX
 XX 07-FEB-2000; 2000US-00499148.
 PF
 XX
 XX 16-AUG-1996; 96US-0024115P.
 PR
 XX 29-APR-1997; 97US-00841035.
 PR
 XX (GEMY) GENETICS INST LLC.
 PA
 XX
 XX Somers WS, Stahl ML, Seehra JS, Xu G, McDonagh TE, Yu H, Hong J;
 PI WPI; 2003-719565/68.
 DR
 XX Crystalline human interleukin-6, useful for identifying IL-6/IL-6
 PT receptor interactions, and for identifying agonists and antagonists of
 PT such interactions, has diffracting crystals of a specific space group.
 XX
 XX Disclosure; SEQ ID NO 4; 30pp; English.
 PS
 XX The invention relates to crystalline human interleukin-6 (IL-6). The
 CC crystalline form of IL-6 is useful for identifying IL-6/IL-6 receptor
 CC interactions, and for identifying agonists and antagonists of the
 CC interactions. Crystalline IL-6 structure enables effective study of its
 CC interactions with its receptor. The present sequence represents the amino
 CC acid sequence of rhesus monkey interleukin-6, IL-6.
 XX
 XX Sequence 166 AA;
 SQ

Query Match 59.2%; Score 61; DB 7; Length 166;
 Best Local Similarity 57.9%; Pred.No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GNETSCLKKLADGFFFE 19
 ||| :|| : |||
 Db 59 GFNETCLVKIITGLEFE 77

Search completed: March 30, 2005, 22:01:42
 Job time : 22.0448 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:58:00 ; Search time 5.02691 Seconds
(without alignments)
282.148 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKKLADGPFEEFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	185	3	US-09-122-443-16
2	103	100.0	185	4	US-09-558-089-16
3	103	100.0	185	4	US-09-558-087-16
4	103	100.0	185	4	US-09-558-474-16
5	103	100.0	204	3	US-09-230-637-25
6	103	100.0	204	3	US-09-230-371A-26
7	61	59.2	89	4	US-09-687-637B-36
8	61	59.2	89	4	US-09-687-637B-37
9	61	59.2	89	4	US-09-687-637B-38
10	61	59.2	162	2	US-08-716-317-10
11	61	59.2	163	2	US-08-716-317-15
12	61	59.2	164	1	US-08-318-193-60
13	61	59.2	166	4	US-09-499-148-1
14	61	59.2	166	4	US-09-499-148-4
15	61	59.2	167	1	US-08-246-427A-2
16	61	59.2	167	2	US-08-766-620-2
17	61	59.2	167	5	PCT-US95-06094-2
18	61	59.2	172	3	US-08-149-101A-21
19	61	59.2	172	5	PCT-US94-12873-21
20	61	59.2	174	3	US-08-149-101A-20
21	61	59.2	174	5	PCT-US94-12873-20
22	61	59.2	183	1	US-08-009-973-1
23	61	59.2	184	1	US-08-567-047-2
24	61	59.2	184	2	US-08-693-182-2
25	61	59.2	184	2	US-08-567-048-2
26	61	59.2	184	2	US-09-008-482-2
27	61	59.2	184	2	US-08-945-529-8

28	61	59.2	184	2	US-08-945-529-9	Sequence 9, Appli
29	61	59.2	184	2	US-08-945-529-10	Sequence 10, Appl
30	61	59.2	184	2	US-08-945-529-11	Sequence 11, Appl
31	61	59.2	184	2	US-08-945-529-12	Sequence 12, Appl
32	61	59.2	184	3	US-08-149-101A-17	Sequence 17, Appl
33	61	59.2	184	3	US-08-149-101A-22	Sequence 22, Appl
34	61	59.2	184	4	US-09-559-950A-1	Sequence 1, Appli
35	61	59.2	184	5	PCT-US94-12873-17	Sequence 17, Appl
36	61	59.2	184	5	PCT-US94-12873-22	Sequence 22, Appl
37	61	59.2	184	6	5186931-1	Patent No. 5186931
38	61	59.2	184	6	5186931-1	Patent No. 5186931
39	61	59.2	185	1	US-07-632-070B-1	Sequence 1, Appli
40	61	59.2	185	1	US-07-918-181A-2	Sequence 2, Appli
41	61	59.2	185	1	US-07-918-181A-4	Sequence 4, Appli
42	61	59.2	185	1	US-07-918-181A-6	Sequence 6, Appli
43	61	59.2	185	1	US-07-918-181A-8	Sequence 8, Appli
44	61	59.2	185	1	US-08-231-575-2	Sequence 2, Appli
45	61	59.2	185	1	US-08-231-575-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-122-443-16
; Sequence 16, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-16

Query Match 100.0%; Score 103; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GFNETSCLKKLADGPFEEFE 19
Db 68 GFNETSCLKKLADGPFEEFE 86

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RESULT 2
US-09-558-089-16
; Sequence 16, Application US/09558089
; Patent No. 6479634
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,089
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/122,443
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-089-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86

RESULT 3
US-09-558-089-16
; Sequence 16, Application US/09558087
; Patent No. 6495667
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-089-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86

RESULT 4
US-09-558-474-16
; Sequence 16, Application US/09558474
; Patent No. 6835825
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/558,474
; FILING DATE: 25-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELEPHONE: (650) 852-9196
; TELEFAX: (650) 496-1200
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-474-16
Query Match 100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGPFPE 19
Db 68 GNETSCLKKLADGPFPE 86
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; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-558-474-16

Query Match      100.0%; Score 103; DB 4; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.4e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 68 GFNETSCLKKLADGFFFE 86

RESULT 5
US-09-230-637-25
; Sequence 25, Application US/09230637
; Patent No. 6264958
; GENERAL INFORMATION:
; APPLICANT: Hayward, Gary
; APPLICANT: Nicholas, John
; APPLICANT: Hardwick, J. Marie
; APPLICANT: Reitz, Marvin
; TITLE OF INVENTION: No. 6264958el Genes of Kaposi's Sarcoma
; FILE REFERENCE: 1107.78372
; CURRENT APPLICATION NUMBER: US/09/230,637
; CURRENT FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/022,591
; PRIOR FILING DATE: 1996-07-25
; PRIOR APPLICATION NUMBER: PCT US 97/12931
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpes-like virus
US-09-230-637-25

Query Match      100.0%; Score 103; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 87 GFNETSCLKKLADGFFFE 105

RESULT 6
US-09-230-371A-26
; Sequence 26, Application US/09230371A
; Patent No. 6348586
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Bohenzky, Roy A
; APPLICANT: Russo, James J
; APPLICANT: Edelman, Isidore S
; APPLICANT: Moore, Patrick S
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
; FILE REFERENCE: 45185-G-PCT-US
; CURRENT APPLICATION NUMBER: US/09/230,371A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US97/13346
; PRIOR FILING DATE: 1997-07-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-230-371A-26

Query Match      100.0%; Score 103; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 87 GFNETSCLKKLADGFFFE 105

RESULT 7
US-09-687-637B-36
; Sequence 36, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Cercosporium torquatus atys
US-09-687-637B-36

Query Match      59.2%; Score 61; DB 4; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 8
US-09-687-637B-37
; Sequence 37, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-687-637B-37

Query Match      59.2%; Score 61; DB 4; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 54 GFNETCLVKIITGLLEFE 72

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RESULT 9
US-09-687-637B-38
; Sequence 38, Application US/09687637B
; Patent No. 6610285
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/09/687,637B
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-687-637B-38

Query Match 59.2%; Score 61; DB 4; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.011;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGFFFE 19
||||:|:|:|
DB 54 GFNEETCLVKIITGLLEFE 72

RESULT 10
US-08-716-317-10
; Sequence 10, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO
; APPLICANT: TOHDA, HIDEKI
; APPLICANT: TSUKAMOTO, HIROKO
; APPLICANT: NIKAIIDO, KIYOKAZU
; APPLICANT: KUMAGAI, HIROMICHI
; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
; TITLE OF INVENTION: VECTOR CONTAINING IT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-716-317-10

Query Match 59.2%; Score 61; DB 2; Length 162;
Best Local Similarity 57.9%; Pred. No. 0.022;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GNETSCLKKLADGFFFE 19
||||:|:|:|
DB 55 GFNEETCLVKIITGLLEFE 73

RESULT 11
US-08-716-317-15
; Sequence 15, Application US/08716317
; Patent No. 5919654
; GENERAL INFORMATION:
; APPLICANT: HAMA, YUKO
; APPLICANT: TOHDA, HIDEKI
; APPLICANT: TSUKAMOTO, HIROKO
; APPLICANT: NIKAIIDO, KIYOKAZU
; APPLICANT: KUMAGAI, HIROMICHI
; TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION
; TITLE OF INVENTION: VECTOR CONTAINING IT
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716,317
FILING DATE: 02-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00198
FILING DATE: 01-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 17167/1995
FILING DATE: 03-FEB-1996
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 59-924-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-317-15

Query Match 59.2%; Score 61; DB 2; Length 163;
Best Local Similarity 57.9%; Pred. No. 0.022;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKLAGDGFPE 19
Db 56 GFNEETCLVKIITGLLEFE 74

RESULT 12

US-08-318-193-60
Sequence 60, Application US/08318193

Patent No. 5641663

GENERAL INFORMATION:

APPLICANT: GARVIN, Robert T.

APPLICANT: MALEK, Lawrence T.

TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/318,193

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,314

FILING DATE:

ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US 07/224,568

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 18740/116 CACO

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:

LENGTH: 164 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-318-193-60

Query Match 59.2%; Score 61; DB 1; Length 164;

Best Local Similarity 57.9%; Pred. No. 0.022;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKLAGDGFPE 19

Db 57 GFNEETCLVKIITGLLEFE 75

RESULT 13

US-09-499-148-1

Sequence 1, Application US/09499148

Patent No. 6461604

GENERAL INFORMATION:

APPLICANT: SOMERS, WILLIAM

APPLICANT: STAHL, MARK L.

APPLICANT: SEEHRA, JASBIR S.

APPLICANT: XU, GUANG-YI

APPLICANT: MCCONAGH, THOMAS E.

APPLICANT: YU, HSIANG-AI

APPLICANT: HONG, JIN

TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6

FILE REFERENCE: 50657-05278USC1

CURRENT APPLICATION NUMBER: US/09/499,148

CURRENT FILING DATE: 2000-02-07

PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115

PRIOR FILING DATE: 1997-4-28 AND 1996-8-16

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 1

LENGTH: 166

TYPE: PRT

ORGANISM: Homo sapiens

US-09-499-148-1

Query Match 59.2%; Score 61; DB 4; Length 166;

Best Local Similarity 57.9%; Pred. No. 0.022;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKLAGDGFPE 19

Db 59 GFNEETCLVKIITGLLEFE 77

RESULT 14

US-09-499-148-4

Sequence 4, Application US/09499148

Patent No. 6461604

GENERAL INFORMATION:

APPLICANT: SOMERS, WILLIAM

APPLICANT: STAHL, MARK L.

APPLICANT: SEEHRA, JASBIR S.

APPLICANT: XU, GUANG-YI

APPLICANT: MCCONAGH, THOMAS E.

APPLICANT: YU, HSIANG-AI

APPLICANT: HONG, JIN

TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6

FILE REFERENCE: 50657-05278USC1

CURRENT APPLICATION NUMBER: US/09/499,148

CURRENT FILING DATE: 2000-02-07

PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115

PRIOR FILING DATE: 1997-4-28 AND 1996-8-16

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.0

SEQ ID NO 4

LENGTH: 166

TYPE: PRT

ORGANISM: Macaca mulatta

US-09-499-148-4

Query Match 59.2%; Score 61; DB 4; Length 166;

Best Local Similarity 57.9%; Pred. No. 0.022;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKLAGDGFPE 19

Db 59 GFNEETCLVKIITGLLEFE 77

RESULT 15

US-08-246-427A-2

Sequence 2, Application US/08246427A

Patent No. 5641657

GENERAL INFORMATION:

APPLICANT: RUBEN, ET AL.

TITLE OF INVENTION: Interleukin-6 Splice Variant

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD

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; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,427A
; FILING DATE: Submitted herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/246,427
; FILING DATE: MAY 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
;
US-08-246-427A-2

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Query Match      59.2%; Score 61; DB 1; Length 167;
Best Local Similarity 57.9%; Pred.No. 0.022;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY      1 GFNETSCLKKLADGFFFE 19
Db      60 GFNETCLVKIITGLLEFE 78

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Search completed: March 30, 2005, 22:11:03
Job time : 6.02691 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 21:49:40 ; Search time 16.1031 Seconds
(without alignments)
390.664 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKKLADGPFPEFE 19

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	59.2	89	14	US-10-440-066-36
2	61	59.2	89	14	US-10-440-066-37
3	61	59.2	89	14	US-10-440-066-38
4	61	59.2	166	14	US-10-246-946-1
5	61	59.2	166	14	US-10-246-946-4
6	61	59.2	183	16	US-10-658-834A-198
7	61	59.2	183	16	US-10-658-834A-217
8	61	59.2	183	16	US-10-658-834A-217
9	61	59.2	183	16	US-10-658-834A-896
10	61	59.2	183	16	US-10-658-834A-897
11	61	59.2	183	16	US-10-658-834A-898
12	61	59.2	183	16	US-10-658-834A-899
13	61	59.2	183	16	US-10-658-834A-900
14	61	59.2	183	16	US-10-658-834A-901

14	59.2	183	16	US-10-658-834A-902	Sequence 902, App
15	59.2	183	16	US-10-658-834A-903	Sequence 903, App
16	59.2	183	16	US-10-658-834A-904	Sequence 904, App
17	59.2	183	16	US-10-658-834A-905	Sequence 905, App
18	59.2	183	16	US-10-658-834A-906	Sequence 906, App
19	59.2	183	16	US-10-658-834A-907	Sequence 907, App
20	59.2	183	16	US-10-658-834A-908	Sequence 908, App
21	59.2	183	16	US-10-658-834A-914	Sequence 914, App
22	59.2	183	16	US-10-658-834A-915	Sequence 915, App
23	59.2	183	16	US-10-658-834A-916	Sequence 916, App
24	59.2	183	16	US-10-658-834A-917	Sequence 917, App
25	59.2	183	16	US-10-658-834A-918	Sequence 918, App
26	59.2	183	16	US-10-658-834A-919	Sequence 919, App
27	59.2	183	16	US-10-658-834A-920	Sequence 920, App
28	59.2	183	16	US-10-658-834A-921	Sequence 921, App
29	59.2	183	16	US-10-658-834A-922	Sequence 922, App
30	59.2	183	16	US-10-658-834A-923	Sequence 923, App
31	59.2	183	16	US-10-658-834A-924	Sequence 924, App
32	59.2	183	16	US-10-658-834A-925	Sequence 925, App
33	59.2	183	16	US-10-658-834A-926	Sequence 926, App
34	59.2	183	16	US-10-658-834A-927	Sequence 927, App
35	59.2	183	16	US-10-658-834A-928	Sequence 928, App
36	59.2	183	16	US-10-658-834A-929	Sequence 929, App
37	59.2	183	16	US-10-658-834A-930	Sequence 930, App
38	59.2	183	16	US-10-658-834A-931	Sequence 931, App
39	59.2	183	16	US-10-658-834A-932	Sequence 932, App
40	59.2	183	16	US-10-658-834A-933	Sequence 933, App
41	59.2	183	16	US-10-658-834A-934	Sequence 934, App
42	59.2	183	16	US-10-658-834A-935	Sequence 935, App
43	59.2	183	16	US-10-658-834A-936	Sequence 936, App
44	59.2	183	16	US-10-658-834A-937	Sequence 937, App
45	59.2	183	16	US-10-658-834A-938	Sequence 938, App

ALIGNMENTS

RESULT 1
US-10-440-066-36
; Sequence 36, Application US/10440066
; Publication No. US20030180256A1
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/440,066
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US/09/687,637
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Cercopithecus torquatus atys
US-10-440-066-36

Query Match 59.2%; Score 61; DB 14; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKKLADGPFPEFE 19
|||||:|:|:|
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 2
US-10-440-066-37
; Sequence 37, Application US/10440066

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; Publication No. US20030180256A1
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/440,066
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US/09/687,637
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-440-066-37

Query Match      59.2%; Score 61; DB 14; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 3
US-10-440-066-38
; Sequence 38, Application US/10440066
; Publication No. US20030180256A1
; GENERAL INFORMATION:
; APPLICANT: Hirata, Yuichi
; TITLE OF INVENTION: CYTOKINE-LIKE PROTEINS THAT PROMOTE CELL PROLIFERATION
; FILE REFERENCE: 06501-067001
; CURRENT APPLICATION NUMBER: US/10/440,066
; CURRENT FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: US/09/687,637
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: PCT/JP99/01997
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: JP 10/121805
; PRIOR FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-066-38

Query Match      59.2%; Score 61; DB 14; Length 89;
Best Local Similarity 57.9%; Pred. No. 0.02;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 54 GFNETCLVKIITGLLEFE 72

RESULT 4
US-10-246-946-1
; Sequence 1, Application US/10246946
; Publication No. US20030068300A1
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: XU, GUANG-YI
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
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```
; APPLICANT: YU, HSIANG-AI
; APPLICANT: HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USD1
; CURRENT APPLICATION NUMBER: US/10/246,946
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 09/499,148, 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-946-1

Query Match      59.2%; Score 61; DB 14; Length 166;
Best Local Similarity 57.9%; Pred. No. 0.041;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 59 GFNETCLVKIITGLLEFE 77

RESULT 5
US-10-246-946-4
; Sequence 4, Application US/10246946
; Publication No. US20030068300A1
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; APPLICANT: HONG, JIN
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USD1
; CURRENT APPLICATION NUMBER: US/10/246,946
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 09/499,148, 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 2000-2-7, 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-246-946-4

Query Match      59.2%; Score 61; DB 14; Length 166;
Best Local Similarity 57.9%; Pred. No. 0.041;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFEE 19
Db 59 GFNETCLVKIITGLLEFE 77

RESULT 6
US-10-658-834A-198
; Sequence 198, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
```

```
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank CAA00839
; DATABASE ENTRY DATE: 1993-12-03
US-10-658-834A-198
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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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Qy 1 GFNETSCLKKLADGFFFE 19
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Db 76 GFNEETCLVKIITGLLEFE 94
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RESULT 7

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US-10-658-834A-217
; Sequence 217, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAD13886
; DATABASE ENTRY DATE: 1993-06-28
US-10-658-834A-217
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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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Qy 1 GFNETSCLKKLADGFFFE 19
||||:|:|:|
Db 76 GFNEETCLVKIITGLLEFE 94
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RESULT 8

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US-10-658-834A-896
; Sequence 896, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
```

```
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-896
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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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Qy 1 GFNETSCLKKLADGFFFE 19
||||:|:|:|
Db 76 GFNEETCLVKIITGLLEFE 94
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RESULT 9

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US-10-658-834A-897
; Sequence 897, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 897
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-897
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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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```
Qy 1 GFNETSCLKKLADGFFFE 19
||||:|:~|:|
Db 76 GFNEETCLVKIITGLLEFE 94
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RESULT 10

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US-10-658-834A-898
; Sequence 898, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
```

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; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 898
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-898

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||: ||: ||||
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 11
US-10-658-834A-899
; Sequence 899, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 899
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-899

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||: ||: ||||
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 12
US-10-658-834A-900
; Sequence 900, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
```

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; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 900
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-900

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||: ||: ||||
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 13
US-10-658-834A-901
; Sequence 901, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-834A-901

Query Match          59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGPFPE 19
    ||||: ||: ||||
Db 76 GFNEETCLVKIITGLLEPE 94

RESULT 14
US-10-658-834A-902
; Sequence 902, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nuc
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; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 902
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-658-834A-902
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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFEFE 19
   ||||:||||:
Db 76 GFNETCLVKIITGLLEFE 94
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RESULT 15
US-10-658-834A-903
; Sequence 903, Application US/10658834A
; Publication No. US20040112977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; TITLE OF INVENTION: Molecules and Related Applications
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-658-834A-903
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Query Match 59.2%; Score 61; DB 16; Length 183;
Best Local Similarity 57.9%; Pred. No. 0.045;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFEFE 19
   ||||:||||:
Db 76 GFNETCLVKIITGLLEFE 94
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Search completed: March 30, 2005, 22:09:56
Job time : 16.1031 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:47:50 ; Search time 4.5157 Seconds
(without alignments)
404.837 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105

Perfect score: 103
Sequence: 1 GFNETSCLKLADGFFFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: piri:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	59.2	212	1 IVHUB2	interleukin-6 prec
2	55	53.4	208	2 T09216	interleukin-6 prec
3	53	51.5	212	2 I46590	interleukin 6 - pi
4	53	51.5	212	2 I46621	prointerleukin 6 -
5	51	49.5	207	2 I46084	interleukin 6 - ca
6	49	47.6	211	2 A34247	interleukin-6 prec
7	48.5	47.1	196	2 C95322	hypothetical prote
8	48	46.6	162	2 H83786	hypothetical prote
9	47	45.6	211	1 ICM86	interleukin-6 prec
10	47	45.6	745	2 T05375	hypothetical prote
11	46	44.7	208	1 S29549	interleukin-6 - sh
12	46	44.7	568	2 C82379	response regulator
13	45	43.7	484	2 F71061	hypothetical prote
14	44	42.7	282	2 D70149	hypothetical prote
15	44	42.7	454	2 T27249	hypothetical prote
16	44	42.7	1893	2 T22661	hypothetical prote
17	44	42.7	2875	1 RRVUTW	genome polyprotein
18	44	42.7	4196	2 T43274	dydin heavy chain
19	43.5	42.2	233	2 AC2205	hypothetical prote
20	43	41.7	157	2 H69203	conserved hypotet
21	43	41.7	208	1 A56610	interleukin-6 prec
22	43	41.7	231	2 H83664	ribosomal protein
23	42.5	41.3	492	2 T30066	hypothetical prote
24	42	40.8	180	2 H72402	hypothetical prote
25	42	40.8	219	2 H88101	protein W09G10.2 [
26	42	40.8	364	2 T23819	hypothetical prote
27	42	40.8	445	2 G98290	hypothetical prote
28	42	40.8	445	2 AC2993	conserved hypotet
29	42	40.8	512	2 S47900	protein kinase RCK

30 42 40.8 861 2 T41945 primase - human he
31 42 40.8 1690 2 T13030 microtubule bindin
32 42 40.8 2048 1 ZLNZSE genome polyprotein
33 42 40.8 2139 2 S46404 vitellogenin - yel
34 42 40.8 2238 1 ZLNZSV genome polyprotein
35 42 40.8 2233 1 ZLNZP3 genome polyprotein
36 41.5 40.3 386 2 E81443 hypohetical prote
37 41 39.8 158 2 T17748 hypohetical prote
38 41 39.8 159 1 E71208 hypohetical prote
39 41 39.8 320 2 S22615 hypohetical prote
40 41 39.8 343 2 JN0249 vancomycin resista
41 41 39.8 689 2 T51220 hypohetical prote
42 41 39.8 787 2 T00798 hypohetical prote
43 41 39.8 1224 2 S25952 gene cob intron 3
44 41 39.8 1642 2 T08880 NMDA receptor-bind
45 40.5 39.3 244 2 JC2425 glutathione transf

ALIGNMENTS

RESULT 1
IVHUB2
Interleukin-6 precursor [validated] - human
N/Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell
on factor
C/Species: Homo sapiens (man)
C/Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C/Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601; B27
R/Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishimoto,
EMBO J. 6, 2939-2945, 1987
A/Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) gene
A/Reference number: A32648; MUID:88082664; PMID:3500852
A/Accession: A32648
A/Molecule type: DNA
A/Residues: 1-212 <YAS>
A/Cross-references: UNIPROT:P05231; GB:Y00081; NID:G29494; PIDN:CAA68278.1; PID:G29495
R/Note: the authors translated the codon CAG for residue 130 as Glu
R/Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A/Title: Structure and expression of cDNA and genes for human interferon-beta-2, a distri
A/Reference number: A91051; MUID:87053818; PMID:3023045
A/Accession: A25692
A/Molecule type: mRNA
A/Residues: 1-212 <ZIL>
A/Cross-references: GB:X04430; NID:G32673; PIDN:CAA28026.1; PID:G32674
R/Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwamura,
i, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A/Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymphocyt
A/Reference number: A93387; MUID:87065033; PMID:3491322
A/Accession: A26966
A/Molecule type: mRNA
A/Residues: 1-212 <HIR>
A/Cross-references: GB:X04602; NID:G33849; PIDN:CAA28268.1; PID:G33850
R/Tonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A/Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of t
A/Reference number: A33515; MUID:89391958; PMID:2789513
A/Accession: A33515
A/Molecule type: mRNA
A/Residues: 1-212 <TON>
A/Cross-references: GB:M29150; NID:G186349; PIDN:AAAS9154.1; PID:G307063
R/Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A/Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h
A/Reference number: A25801; MUID:87004683; PMID:3758081
A/Accession: A25801
A/Molecule type: DNA: mRNA
A/Residues: 1-212 <HAE>
A/Cross-references: GB:X04403
A/Experimental source: fibroblast
R/May, L.T.; Helfgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A>Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433; PMID:3538015
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAY>
 A:Cross-references: GB:M14584; NID:g184628; PIDN:AA52728.1; PID:g306910
 R:Wong, G.G.; Witek-Giannotti, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Mitt. 83, 40-47, 1988
 A>Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: I52193; MUID:89193317; PMID:3266463
 A:Accession: I52193
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <NON>
 A:Cross-references: GB:M54894; NID:g186351; PIDN:AA41704.1; PID:g186352
 R:Brakenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A>Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli
 A:Reference number: I56003; MUID:88088768; PMID:3320204
 A:Accession: I56003
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: protein
 A:Residues: 1-212 <BRA>
 A:Cross-references: GB:M18403; NID:g184631; PIDN:AA52729.1; PID:g306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A>Title: Separation and comparison of two monokines with lymphocyte-activating factor activity
 A:Reference number: A92816; MUID:88154445; PMID:3279116
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VAN1>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved in cell growth and differentiation
 A:Reference number: A60400; MUID:90171574; PMID:2307841
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and its cDNA
 A:Reference number: A29085; MUID:87092370; PMID:3491991
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Aizawa, H.
 Anticancer Res. 11, 961-968, 1991
 A>Title: Purification and characterization of human fibroblast derived differentiation factor
 A:Reference number: A61159; MUID:91290785; PMID:1648338
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NOD>
 A:Experimental source: fibroblast
 R:Ming, J.E.; Cernetti, C.; Steinman, R.M.; Granelli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A>Title: Interleukin 6 is the principal cytokine for T lymphocyte differentiation factor for T cell growth and differentiation
 A:Reference number: A61462; MUID:90121567; PMID:2610854
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabriskie, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A>Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Reference number: A48419; MUID:91355644; PMID:1883960
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAY2>
 A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
 A>Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K form cc
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAY3>
 A:Experimental source: FS-4 fibroblasts
 A>Note: sequence extracted from NCBI backbone (NCBIP:63787)
 A>Note: this 23-25K form contained O-linked but not N-linked carbohydrate
 R:Orlita, T.; Oneda, M.; Hasegawa, M.; Kuboniwa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 produced in CHO cells
 A:Reference number: JX0305; MUID:94266765; PMID:8206884
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human interleukin-6 are similar to those of human granulocyte-macrophage colony-stimulating factor
 A:Reference number: S04981; MUID:89286115; PMID:2472117
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ida, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044; PMID:8172889
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth factors (IL-1, IL-3, IL-6, IL-11, IL-12, IL-13, IL-15, IL-18, IL-21, IL-23, IL-25, IL-27, IL-28, IL-29, IL-30, IL-31, IL-32, IL-33, IL-34, IL-35, IL-36, IL-37, IL-38, IL-39, IL-40, IL-41, IL-42, IL-43, IL-44, IL-45, IL-46, IL-47, IL-48, IL-49, IL-50, IL-51, IL-52, IL-53, IL-54, IL-55, IL-56, IL-57, IL-58, IL-59, IL-60, IL-61, IL-62, IL-63, IL-64, IL-65, IL-66, IL-67, IL-68, IL-69, IL-70, IL-71, IL-72, IL-73, IL-74, IL-75, IL-76, IL-77, IL-78, IL-79, IL-80, IL-81, IL-82, IL-83, IL-84, IL-85, IL-86, IL-87, IL-88, IL-89, IL-90, IL-91, IL-92, IL-93, IL-94, IL-95, IL-96, IL-97, IL-98, IL-99, IL-100, IL-101, IL-102, IL-103, IL-104, IL-105, IL-106, IL-107, IL-108, IL-109, IL-110, IL-111, IL-112, IL-113, IL-114, IL-115, IL-116, IL-117, IL-118, IL-119, IL-120, IL-121, IL-122, IL-123, IL-124, IL-125, IL-126, IL-127, IL-128, IL-129, IL-130, IL-131, IL-132, IL-133, IL-134, IL-135, IL-136, IL-137, IL-138, IL-139, 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QY 1 GFNETSCLKKLADGFFPEF 19
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Db 102 GFNQETCLMKITITGLSEFQ 120

RESULT 3

I46590
interleukin 6 - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: I46590
R/Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A/Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation conceptuses
A/Reference number: I46590; MUID:92360284; PMID:1497880
A/Accession: I46590
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-212 <MAT>
A/Cross-references: UNIPROT:P26893; GB:M80258; NID:g164514; PIDN:AAAC27127.1; PID:g164514
C/Genetics:
A/Gene: IL-6
C/Superfamily: interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
Best Local Similarity 42.1%; Pred. No. 0.51;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFPEF 19
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Db 105 GFNQETCLMKITITGLSEFQ 123

RESULT 4

I46621
prointerleukin 6 - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C/Accession: I46621
R/Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A/Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of the cDNA
A/Reference number: I46621; MUID:91338547; PMID:1873476
A/Accession: I46621
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-212 <R1C>
A/Cross-references: UNIPROT:P26893; GB:M86722; NID:g164624; PIDN:AAAC37333.1; PID:g164624
C/Genetics:
A/Gene: IL6
C/Superfamily: interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
Best Local Similarity 42.1%; Pred. No. 0.51;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFPEF 19
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Db 105 GFNQETCLMKITITGLSEFQ 123

RESULT 5

I46084
interleukin 6 - cat
C/Species: Felis silvestris catus (domestic cat)
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: I46084
R/Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993
A/Title: Molecular cloning and characterization of a cDNA encoding feline interleukin-6.
A/Reference number: I46084; MUID:94052249; PMID:8524373
A/Accession: I46084
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA
A/Residues: 1-207 <BRA>
A/Cross-references: UNIPROT:P41683; GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520
C/Superfamily: interleukin-6

Query Match 49.5%; Score 51; DB 2; Length 207;
Best Local Similarity 42.1%; Pred. No. 1;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFPEF 19
||||: ||| |
Db 101 GFNQETCLTRITGLQEFQ 119

RESULT 6

A34247
interleukin-6 precursor - rat
N/Alternate names: IL-6
C/Species: Rattus norvegicus (Norway rat)
C/Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 09-Jul-2004
C/Accession: A34247
R/Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A/Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derived cells
A/Reference number: A34247; MUID:89380206; PMID:2789217
A/Accession: A34247
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-211 <NOR>
A/Cross-references: UNIPROT:P20607; GB:M26744; NID:g204915; PIDN:AAA77659.1; PID:g204916
C/Superfamily: interleukin-6
C/Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 47.6%; Score 49; DB 2; Length 211;
Best Local Similarity 44.4%; Pred. No. 2.2;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFPEF 18
|||: ||| |
Db 103 GYNQETCLLKICSGLLEF 120

RESULT 7

C95322
hypothetical protein Sma0882 [imported] - Sinorhizobium meliloti (strain 1021) magaplasmi
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C/Accession: C95322
R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse, J.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Welle, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A/Reference number: A95262; MUID:21396509; PMID:11481432
A/Accession: C95322
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-196 <KUR>
A/Cross-references: UNIPROT:Q92ZK2; GB:AE006469; PIDN:AAK65141.1; PID:g145233582; GSPDB:G7
A/Experimental source: strain 1021, megaplasmid pSymb
R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Hymann, R.W.; Jones, T.; Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, M.; Hebut, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.; A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
A/Contents: annotation
C/Genetics:
A/Gene: Sma0882
A/Genome: plasmid

Query Match 47.1%; Score 48.5; DB 2; Length 196;

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Best Local Similarity 58.8%; Pred. No. 2.5;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 FNETSCLKKLADGFFEF 18
DB 86 FNSNRCL-IADGFEVF 101

RESULT 8
H83786
hypothetical protein BH1096 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
A:Accession: H83786
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H83786
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <STO>
A:Cross-references: UNIPROT:Q9KDW5; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BA048
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1096

Query Match 46.6%; Score 48; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 TSCLKKLADGFFEEF 19
DB 31 TSMIEIGADGFFEEF 45

RESULT 9
ICWS6
interleukin-6 precursor - mouse
A:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocy
acytoma growth factor
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
A:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S10
R:Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of potentia
A:Reference number: A30531; MUID:89035525; PMID:3263439
A:Accession: A30531
A:Molecule type: DNA
A:Residues: 1-211 <TAN>
A:Cross-references: UNIPROT:P08505; GB:M20572; NID:g341131; PIDN:AAA39302.1; PID:g387386
R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim
Eur. J. Immunol. 18, 193-197, 1988
A:Title: cDNA cloning of murine interleukin-HPL: homology with human interleukin 6.
A:Reference number: A27610; MUID:88166883; PMID:2965020
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <VAN>
A:Cross-references: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702
R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla
J. Immunol. 142, 1372-1376, 1989
A:Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MUID:89124383; PMID:2563387
A:Accession: A30571
A:Molecule type: mRNA
A:Residues: 5-211 <MOC>
A:Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A:Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
A:Reference number: S01323; MUID:88329059; PMID:3262059
A:Accession: S01323

```

```

A:Molecule type: protein
A:Residues: 25-166, 'X', 168-211 <SIM>
A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A-
R:Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A:Reference number: S12103; MUID:91057159; PMID:2243807
A:Accession: S12103
A:Molecule type: mRNA
A:Residues: 1-211 <GRE>
A:Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A:Reference number: A90157; MUID:90147691; PMID:2302197
A:Accession: E34047
A:Molecule type: protein
A:Residues: 66-69, 'X', 71-75; 78-94; 128-148 <JA5>
R:Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; Simp
Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
A:Reference number: A26662; MUID:87092311; PMID:2948184
A:Accession: A26662
A:Molecule type: protein
A:Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
A:Reference number: A40486; MUID:89017145; PMID:3262872
A:Accession: A40486
A:Molecule type: mRNA
A:Residues: 1-211 <CHI>
A:Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
Blood 72, 2070-2073, 1988
A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6.
A:Reference number: A60799; MUID:89062753; PMID:3264198
A:Accession: A60799
A:Molecule type: protein
A:Residues: 77-98 <SHA>
R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mo
A:Reference number: S10241; MUID:90171860; PMID:2106569
A:Accession: S10241
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <BLA>
A:Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860
R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 217, 53-59, 1993
A:Title: Specific covalent modification of the tryptophan residues in murine interleukin-
A:Reference number: S38254; MUID:94039075; PMID:8223586
A:Accession: S38254
A>Status: preliminary
A:Molecule type: protein
A:Residues: 38-60; 75, 'X', 77-79; 176-203 <ZHA>
C:Genetics:
A:Gene: IL-6
A:Map position: 5
A:Introns: 7/1; 68/3; 106/3; 156/3
C:Superfamily: interleukin-6
C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine; n
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-211/Product: interleukin-6 #status experimental <MAT>

Query Match 45.6%; Score 47; DB 1; Length 211;
Best Local Similarity 38.9%; Pred. No. 4.7;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFEF 18
DB 103 GYNQICLLKITSGLLEY 120

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C:Genetics:
A:Gene: VCAI086
A:Map position: 2
C:Superfamily: response regulator, Hnr type; response regulator homology

Query Match 44.7%; Score 46; DB 2; Length 568;
Best Local Similarity 69.2%; Pred. No. 18;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 SCLKKLADGFFEF 18
DB 460 SSLKETPDGFFEF 472
|||: |||||
|||: |||||

RESULT 13
F71061
hypothetical protein PH1188 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: F71061
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekinaka, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon.
A:Reference number: A71000; PMID:98344137; PMID:9679194
A:Accession: F71061
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-484 <KAW>
A:CROSS-references: UNIPROT:O58908; GB:AP000005; NID:g3236132; PIDN:BAA30288.1; PID:d103
A:Experimental source: strain OJ3
A>Note: This accession replaces an interim accession for a sequence replaced by GenBank C:Genetics:
A:Gene: PH1188

Query Match 43.7%; Score 45; DB 2; Length 484;
Best Local Similarity 33.3%; Pred. No. 23;
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFEF 18
DB 75 GYGKTSIMRAEGIIYD 92
||: || :||: ||: ||:
||: || :||: ||: ||:

RESULT 14
D70149
hypothetical protein BB0397 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70149
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, son, D.; Peterson, J.; Kralavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujita, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A>Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; PMID:98065943; PMID:9403685
A:Accession: D70149
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-282 <KLE>
A:CROSS-references: UNIPROT:O51358; GB:AE001145; GB:AE000783; NID:g2688298; PIDN:AAC6677
A:Experimental source: strain B31

Query Match 42.7%; Score 44; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 19;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 FNETSCLKKLADGFF 16
DB 177 YNNTSGSKLEDSEFF 191
:||| ||||| |||||
:||| ||||| |||||

```

RESULT 15
T27249
hypothetical protein Y5F2A.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27249
R:Lennard, N.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20331
A:Accession: T27249
A>Status: preliminary; translated from GB/EMBL/DBSJ
A:Molecule type: DNA
A:Residues: 1-454 <WIL>
A:Cross-references: UNIPROT:Q9XWL0; EMBL:AL032641; PIDN:CAA21647.1; GSPDB:GN000022; CESP:
A:Experimental source: clone Y5F2A
C:Genetics:
A:Gene: CESP:Y5F2A.4
A:Map position: 4
A:Introns: 17/2; 50/3; 125/3; 159/3; 201/3; 241/2; 353/1; 411/1
Query Match 42.7%; Score 44; DB 2; Length 454;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;
QY 3 NETSCLKKLA-----DGFF 16
Db 177 HETSLKRRFAFVCKPCDSYF 196

Search completed: March 30, 2005, 22:06:43
Job time : 5.5157 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 21:12:44 ; Search time 19.9372 Seconds
(without alignments)
488.007 Million cell updates/sec

Title: US-10-828-343-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCLKKLADGFFFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	204	2	O40918 human herpe
2	103	100.0	204	2	O98823 human herpe
3	103	100.0	204	2	O768K3 human herpe
4	62	60.2	160	2	O97535 actus vocif
5	62	60.2	175	2	O97TH4 actus nigri
6	62	60.2	212	2	O8MKH0 salmimiri sci
7	61	59.2	209	2	O97540 actus nancy
8	61	59.2	209	2	O97TH3 actus lemur
9	61	59.2	212	1	IL6 CERTO
10	61	59.2	212	1	IL6 HUMAN
11	61	59.2	212	1	IL6 MACFA
12	61	59.2	212	1	IL6 MACMU
13	58	56.3	241	2	O90Y10 gallus gall
14	55	53.4	208	1	IL6 HORSE
15	54	52.4	209	1	IL6 PHOVI
16	53	51.5	207	1	IL6 CANFA
17	53	51.5	207	2	O9MYZ7 canis fami
18	53	51.5	212	1	IL6 FIG
19	53	51.5	212	2	O8MJ75 sus scrofa
20	53	51.5	214	2	O8MKES sus scrofa
21	52	50.5	211	1	IL6 LAMGL
22	52	50.5	211	2	O865W7 camelus bac
23	52	50.5	892	2	O8L281 proteus vul
24	51	49.5	108	2	O9BDL5 phocoenoide
25	51	49.5	205	1	IL6 ORCOR
26	51	49.5	208	1	IL6 FELCA
27	51	49.5	208	2	O9XT80 delphinapte
28	49	47.6	207	2	O9JHH3 marmota mon
29	49	47.6	211	1	IL6 RAT
30	48.5	47.1	196	2	O92ZK2 rattus norv
31	48	46.6	162	2	O9KDW5 bacillus ha

32	48	46.6	207	1	IL6 MARMO
33	48	46.6	244	2	O6Q4I4
34	48	46.6	628	2	O96XT2
35	47	45.6	211	1	IL6 MOUSE
36	47	45.6	745	2	O81733
37	46	44.7	186	2	O6PZ57
38	46	44.7	208	1	IL6 CAPHI
39	46	44.7	208	1	IL6 SHEEP
40	46	44.7	568	2	O9KKL7
41	46	44.7	904	2	O7NAW9
42	45.5	44.2	492	1	RP54 SHEVI
43	45	43.7	148	2	O9XRE6
44	45	43.7	191	2	O7X0L4
45	45	43.7	207	2	O28403

ALIGNMENTS

RESULT 1
O40918
ID O40918 PRELIMINARY; PRT; 204 AA.
AC O40918;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE OSF K2.
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97138401; PubMed=8985427;
RA Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RT "Human herpesvirus 8 encodes a homolog of interleukin-6.";
RL J. Virol. 71:839-842(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97296220; PubMed=9151804;
RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93872; AAB62676.2; -;
DR GO; U93872; AAB62676.2; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6GCSFMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 204 AA; 23407 MW; 2F467378200D20B9 CRC64;

Query Match 100.0%; Score 103; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
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DB 87 GFNETSCLKKLADGFFFE 105

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RESULT 2
Q98823 ID Q98823 PRELIMINARY; PRT; 204 AA.
AC Q98823;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-6 homolog (Fragment).
GN Name=IL-6;
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.-C., Ensser A., Huang Y.-Q., Li J.J.,
RA Friedman-Klen A.-B., Fleckenstein B.;
RT "Human herpesvirus 8 encodes a homologue of interleukin-6.";
RL J. Virol. 0:0-0(1996).
DR EMBL; U73655; AAB18244.1; -.
DR PDB; 1IIR; X-ray; B=..
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
FT NON TER 204
SQ SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;

Query Match 100.0%; Score 103; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 87 GFNETSCLKKLADGFFFE 105

RESULT 3
Q76SK3 ID Q76SK3 PRELIMINARY; PRT; 204 AA.
AC Q76SK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE ORF K2; functional interleukin-6 vIL-6 homolog (Putative interleukin 6).
OS Human herpesvirus 8 (HHV-8) (Kaposi's sarcoma-associated herpesvirus).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97184526; PubMed=9032328;
RA Nicholas J., Ruvolo V., Zong J., Ciuffo D., Guo H.G., Reitz M.S.,
RA Hayward G.S.;
RT "A single 13-kilobase divergent locus in the Kaposi sarcoma-associated herpesvirus (human herpesvirus 8) genome contains nine open reading frames that are homologous to or related to cellular proteins.";
RL J. Virol. 71:1963-1974(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97208913; PubMed=9055855;
RA Nicholas J., Ruvolo V.R., Burns W.H., Sandford G., Wan X., Ciuffo D.,
RA Hendrickson S.B., Guo H.G., Hayward G.S., Reitz M.S.;

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RT "Kaposi's sarcoma-associated human herpesvirus-8 encodes homologues of
RT macrophage inflammatory protein-1 and interleukin-6.";
RL Nat. Med. 3:287-292(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Sun R., Lin S.-F., Miller G.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97094384; PubMed=8939871; DOI=10.1126/science.274.5293.1739;
RA Moore P.S., Boshoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=97121480; PubMed=8962146; DOI=10.1073/pnas.93.25.14862;
RA Russo J.J., Bohenzky R.A., Chien M.-C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U67774; AAB61701.1; -.
DR EMBL; U71365; AAC34937.1; -.
DR EMBL; U75698; AAC57089.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005125; F:cytokine activity; IEA.
DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6 MGF GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;

Query Match 100.0%; Score 103; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4.7e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
DB 87 GFNETSCLKKLADGFFFE 105

RESULT 4
O97535 ID O97535 PRELIMINARY; PRT; 160 AA.
AC O97535;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-6 (Fragment).
GN Name=IL-6;
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murillo L.A., Patarroyo M.E.;
RT "Identification, cloning, and sequencing of different cytokine genes
RT in four species of owl monkey.";

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RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF014505; AAD01531.1; -.
 DR HSSP; P05231; IL6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT NON TER 1
 SQ SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;

Query Match 60.2%; Score 62; DB 2; Length 160;
 Best Local Similarity 57.9%; Pred. No. 0.11;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKKLADGFFFE 19
 ||||: |||: |||

Db 105 GFNEETCLLKITTGLLEFE 123

RESULT 5

Q9TH4 Q9TH4 PRELIMINARY; PRT; 175 AA.
 AC Q9TH4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 GN Name=IL6;
 OS Aotus nigriceps (Black-headed owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
 RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Patarroyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey."
 RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF097322; AAF21297.1; -.
 DR HSSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 FT NON TER 1
 SQ SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CRC64;

Query Match 60.2%; Score 62; DB 2; Length 175;
 Best Local Similarity 57.9%; Pred. No. 0.12;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKKLADGFFFE 19
 ||||: |||: |||

Db 105 GFNEETCLLKITTGLLEFE 123

RESULT 6

Q8MKH0 Q8MKH0 PRELIMINARY; PRT; 212 AA.
 AC Q8MKH0;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
 RA Heraud J.M., Laverne A., Kazanji M.;
 RT "Molecular cloning, characterization, and quantification of squirrel
 monkey (Saimiri sciureus) Th1 and Th2 cytokines."
 RL Immunogenetics 54:20-29(2002).
 DR EMBL; AF294757; AAK92044.1; -.
 DR HSSP; P05231; IL6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 SQ SEQUENCE 212 AA; 23581 MW; FF22CBF493245479 CRC64;

Query Match 60.2%; Score 62; DB 2; Length 212;
 Best Local Similarity 57.9%; Pred. No. 0.14;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GFNETSCLKKLADGFFFE 19
 ||||: |||: |||

Db 105 GFNEETCLLKITTGLLEFE 123

RESULT 7

O97540 O97540 PRELIMINARY; PRT; 209 AA.
 AC O97540;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin-6 (Fragment).
 GN Name=IL-6;
 OS Aotus nancymae (Ma's night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_TaxID=37293;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
 RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
 RA Murillo L.A., Patarroyo M.E.;
 RT "Identification, cloning, and sequencing of different cytokine genes
 in four species of owl monkey."
 RL Immunogenetics 54:645-653(2002).
 DR EMBL; AF014510; AAD01536.1; -.
 DR HSSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.

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DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 59.2%; Score 61; DB 2; Length 209;
Best Local Similarity 57.9%; Pred. No. 0.2;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 105 GFNETCLVKIITGLLEFE 123

RESULT 8
O9TH3 PRELIMINARY; PRT; 209 AA.
AC O9TH3
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Interleukin-6 (Fragment).
GN Name=IL-6;
QS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22354194; PubMed=12468997; DOI=10.1007/s00251-002-0512-2;
RA Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA Murrillo L.A., Patarroyo M.E.,
RT "Identification, cloning, and sequencing of different cytokine genes
in four species of owl monkey."
RL Immunogenetics 54:645-653(2002).
DR EMBL; AF097323; AAF21298.1; -.
DR HSSP; P05231; 1ALU.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0005125; F:cytokine activity; IEA.
DR GO: GO:0005138; F:interleukin-6 receptor binding; IEA.
DR GO: GO:0008955; P:immune response; IEA.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;

Query Match 59.2%; Score 61; DB 2; Length 209;
Best Local Similarity 57.9%; Pred. No. 0.2;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 105 GFNETCLVKIITGLLEFE 123

us-10-828-343-2_copy_87_105.rup
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RESULT 9
IL6_CERTO STANDARD; PRT; 212 AA.
AC P46650;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FUJ;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
functions: it plays an essential role in the final differentiation
of B-cells into Ig-secreting cells, it induces myeloma and
plasmacytoma growth, it induces nerve cells differentiation, in
hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
with the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL; L26032; AAA99972.1; -.
DR HSSP; P05231; 1ALU.
DR InterPro: IPR009079; 4_helix_cytokine.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 212 AA; 23668 MW; C73C035226B4B9F CRC64;

Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.21;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFFE 19
Db 105 GFNETCLVKIITGLLEFE 123

RESULT 10
IL6_HUMAN STANDARD; PRT; 212 AA.
AC P05231; Q9UCU2; Q9UCU3; Q9UCU4;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
```


25-OCT-2004 (Rel. 45, Last annotation update)
 Interleukin-6 precursor (IL-6) (B-cell stimulatory factor 2) (BSF-2)
 (Interferon beta-2) (Hybridoma growth factor) (CTL differentiation
 factor) (CDF).
 Name=IL6; Synonyms=IFNB2;
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 MEDLINE=87065033; PubMed=3491322;
 Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
 Kashiwamura S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunasawa S.,
 Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
 B lymphocytes to produce immunoglobulin.";
 Nature 324:73-76(1986).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=88082664; PubMed=3500852;
 Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
 Nakai S., Kishimoto T.;
 "Structure and expression of human B cell stimulatory factor-2 (BSF-
 2/IL-6) gene.";
 EMBO J. 6:2939-2945(1987).
 [3]
 SEQUENCE FROM N.A.
 MEDLINE=87067433; PubMed=3538015;
 May L.T., Helfgott D.C., Sehgal P.B.;
 "Anti-beta-interferon antibodies inhibit the increased expression of
 HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 structural studies of the beta 2 interferon involved.";
 Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 [4]
 SEQUENCE FROM N.A.
 MEDLINE=87053818; PubMed=3023045;
 Zilberstein A., Ruggieri R., Korn J.H., Revel M.;
 "Structure and expression of cDNA and genes for human interferon-beta-
 2, a distinct species inducible by growth-stimulatory cytokines.";
 EMBO J. 5:2529-2537(1986).
 [5]
 SEQUENCE FROM N.A.
 MEDLINE=88089768; PubMed=3320204;
 Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 Aarden L.A.;
 "Molecular cloning and expression of hybridoma growth factor in
 Escherichia coli.";
 J. Immunol. 139:4116-4121(1987).
 [6]
 SEQUENCE FROM N.A.
 MEDLINE=89391959; PubMed=2789513;
 Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
 "Deletion of 3' untranslated region of human BSP-2 mRNA causes
 stabilization of the mRNA and high-level expression in mouse NIH3T3
 cells.";
 J. Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 [7]
 SEQUENCE FROM N.A.
 TISSUE=Fibroblast;
 MEDLINE=87004683; PubMed=3758081;
 Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 Fiers W.;
 "Structural analysis of the sequence coding for an inducible 26-kDa
 protein in human fibroblasts.";
 Eur. J. Biochem. 159:625-632(1986).
 [8]
 SEQUENCE FROM N.A.
 MEDLINE=8919317; PubMed=3266463;
 Wong G., Witek-Giannotti J., Hewick R., Clark S., Ogawa M.;
 "Interleukin 6: identification as a hematopoietic colony-stimulating
 factor.";
 Behring Inst. Mitt. 83:40-47(1988).
 RX

[9]
 SEQUENCE FROM N.A.
 MEDLINE=93178270; PubMed=1291290;
 Chen Q.Y.;
 "Stable and efficient expression of human interleukin-6 cDNA in
 mammalian cells after gene transfer.";
 Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 [10]
 SEQUENCE FROM N.A., AND VARIANTS SER-32 AND VAL-162.
 Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Yi Q.,
 Nickerson D.A.;
 "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-
 FHCRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
 Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [11]
 SEQUENCE FROM N.A.
 TISSUE=Lung;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant I.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smallos D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [12]
 SEQUENCE OF 30-63.
 MEDLINE=88154445; PubMed=3279116;
 van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 Billiau A.;
 "Separation and comparison of two monokines with lymphocyte-activating
 factor activity: IL-1 beta and hybridoma growth factor (HGF)."
 Identification of leukocyte-derived HGF as IL-6.";
 J. Immunol. 140:1534-1541(1988).
 [13]
 SEQUENCE OF 30-50.
 MEDLINE=90121567; PubMed=2610854;
 Ming J.E., Cernetti C., Steinman R.M., Granelli-Piperno A.;
 "Interleukin 6 is the principal cytolytic T lymphocyte differentiation
 factor for thymocytes in human leukocyte conditioned medium.";
 J. Mol. Cell. Immunol. 4:203-211(1989).
 [14]
 SEQUENCE OF 30-40, AND GLYCOSYLATION.
 MEDLINE=91355644; PubMed=1883960; DOI=10.1016/1043-4666(91)90018-9;
 May L.T., Shaw J.E., Khanna A.K., Zabriskie J.B., Sehgal P.B.;
 "Marked cell-type-specific differences in glycosylation of human
 interleukin-6.";
 Cytokine 3:204-211(1991).
 [15]
 SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING FIRST DISULFIDE BOND.
 MEDLINE=95154344; PubMed=7851440;
 Breton J., la Fiura A., Bertolero F., Orsini G., Valsasina B.,
 Ziliotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
 "Structure, stability and biological properties of a N-terminally
 truncated form of recombinant human interleukin-6 containing a single
 disulfide bond.";
 Eur. J. Biochem. 227:573-581(1995).
 [16]
 DISULFIDE BONDS.
 MEDLINE=89286115; PubMed=2472117;
 RX

RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RT "Diuflide structures of human interleukin-6 are similar to those of
RT Arch. Biochem. Biophys. 272:144-151(1989).
RN [17]
RP MUTAGENESIS.
RX MEDLINE=91243808; PubMed=2037043; DOI=10.1016/0014-5793(91)80491-K;
RA Lueticken C., Kruetgen A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an alpha-helical
RT structure of the C-terminus for biological activity of human IL-6";
RL FEBS Lett. 282:265-267(1991).
RN [18]
RP STRUCTURE BY NMR.
RX MEDLINE=96134845; PubMed=8555185; DOI=10.1021/bi951949e;
RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
RT by NMR spectroscopy";
RL Biochemistry 35:273-281(1996).
RN [19]
RP STRUCTURE BY NMR.
RX MEDLINE=97303053; PubMed=9159484; DOI=10.1006/jmbi.1997.0933;
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6";
RL J. Mol. Biol. 268:468-481(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=97224126; PubMed=9118960; DOI=10.1093/emboj/16.5.989;
RA Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling";
RL EMBO J. 16:989-997(1997).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: N- and O-glycosylated.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.
CC -!- DATABASE: NAME=RED Systems, cytokine mini-reviews: IL6;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=208".

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Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.21;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKLADGFFFEPE 19
|||:|:|:|
DB 105 GFNETCLVKIITGLLEFE 123

RESULT 11

IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.

OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tateumi M.;
RT "Molecular cloning and expression of cynomolgus monkey interleukin-
RT 6";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.

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DR HSP; AB000554; BAA19148.1; -;
DR HSP; P05231; 1IL6.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN6.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 By similarity.
FT CHAIN 30 212 Interleukin-6.
FT DISULFID 72 78 By similarity.
FT DISULFID 101 111 By similarity.
FT CARBOHYD 73 73 N-linked (GLCNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GLCNAc...) (Potential).
SQ SEQUENCE 212 AA; 23654 MW; CF8173CFBF0B0389 CRC64;

Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.21;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKLADGFFFEPE 19
|||:|:|:|
DB 105 GFNETCLVKIITGLLEFE 123

RESULT 12

IL6_MACMU STANDARD; PRT; 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN Name=IL6;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAC 2;
RX MEDLINE=96003435; PubMed=7561102;
RA Villingier F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";

RL J. Immunol. 155:3946-3954 (1995).
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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 CC
 DR EMBL; L26028; RAA99978.1; --
 DR HSP; P05231; IALU.
 DR InterPro; IPR009079; 4 helix cytokine.
 DR InterPro; IPR003573; IL6_MGF_GCSF.
 DR InterPro; IPR003574; Interleukin_6.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 By similarity.
 FT CHAIN 30 212 Interleukin-6.
 FT DISULFID 72 78 By similarity.
 FT DISULFID 101 111 By similarity.
 FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 212 AA; 23728 MW; 4130DF0CF0BCCAD CRC64;
 Query Match 59.2%; Score 61; DB 1; Length 212;
 Best Local Similarity 57.9%; Pred. No. 0.21;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 105 GFNETCLVXIITGLLEF 123
 ID Q90Y10 PRELIMINARY; PRT; 241 AA.
 AC Q90Y10; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Interleukin-6 precursor.
 GN Names=IL-6;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schneider K., Klaas R., Kaspers B., Staeheli P.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kaiser P., Rothwell L., Galyov E.E., Barrow P.A., Burnside J.,
 RA Wigley P.;
 RT "Differential cytokine expression in avian cells in response to
 RT invasion by Salmonella typhimurium, Salmonella enteritidis and
 RT Salmonella gallinarum."; Microbiology 146:3217-3226 (2000).
 RN [3]

RP SEQUENCE FROM N.A.
 RA Kaiser P.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ309540; CAC40812.1; --
 DR EMBL; AJ250838; CAC15566.2; --
 DR HSP; P05231; IALU.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005125; F:cytokine activity; IEA.
 DR GO; GO:0005138; F:interleukin-6 receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR ProDom; PD004356; Interleukin_6; 1.
 DR SMART; SM00126; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KW Signal.
 FT SIGNAL 1 47 Potential.
 FT CHAIN 48 241 mature ChIL-6.
 SQ SEQUENCE 241 AA; 26790 MW; 657F8049F25BD2F8 CRC64;
 Query Match 56.3%; Score 58; DB 2; Length 241;
 Best Local Similarity 52.8%; Pred. No. 0.7;
 Matches 10; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKKLADGFFFE 19
 DB 126 GFDEKCLTKLSGLFAFQ 144
 ID IL6 HORSE STANDARD; PRT; 208 AA.
 AC Q95181; O19007; O46568;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Interleukin-6 precursor (IL-6).
 GN Names=IL6;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20579380; PubMed-11137120; DOI=10.1016/S0165-2427(00)00241-5;
 RA Swiderski C.E., Sobol G., Lunn D.P., Horohov D.W.;
 RT "Molecular cloning, sequencing, and expression of equine interleukin-6.";
 RT Vet. Immunol. Immunopathol. 77:213-220 (2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
 RT "Molecular cloning of equine interleukin-6.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lai A.C.K.;
 RT "Cloning and expression of equine interleukin-6.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL-6 is a cytokine with a wide variety of biological
 CC functions: it plays an essential role in the final differentiation
 CC of B-cells into Ig-secreting cells, it induces myeloma and
 CC plasmacytoma growth, it induces nerve cells differentiation, in
 CC hepatocytes it induces acute phase reactants (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-6 superfamily.
 CC
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CC -----

DR EMBL; U64794; AAB87703.1; -.
DR EMBL; AF005227; AAB62246.1; -.
DR EMBL; AF041975; AAC04574.1; -.
DR PIR; T09216; T09216.
DR HSSP; P05231; 1IL6.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 208 Interleukin-6.
FT DISULFID 69 75 By similarity.
FT DISULFID 98 108 By similarity.
FT CARBOHYD 71 71 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).
FT CONFLICT 4 5 LS -> FF (in Ref. 1).
FT CONFLICT 8 8 T -> A (in Ref. 3).
FT CONFLICT 137 137 I -> V (in Ref. 2).
FT CONFLICT 205 205 V -> I (in Ref. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 53.4%; Score 55; DB 1; Length 208;
Best Local Similarity 47.4%; Pred.No. 1.8;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKKLADGFFFE 19
DB 102 GFNETCLMKITGLSEFQ 120
||||: |||: |||:
102 GFNETCLMKITGLSEFQ 120

RESULT 15
IL6 PHOVI
ID IL6 PHOVI STANDARD; PRT; 209 AA.
AC Q28519.
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-6 precursor (IL-6) (Fragment).
GN Name=IL6;
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817; DOI=10.1007/s002510050045;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hammi K.D.,
RA Stott J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -!- FUNCTION: IL-6 is a cytokine with a wide variety of biological
CC functions: it plays an essential role in the final differentiation
CC of B-cells into Ig-secreting cells, it induces myeloma and
CC plasmacytoma growth, it induces nerve cells differentiation, in
CC hepatocytes it induces acute phase reactants (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.

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DR EMBL; L46802; AAB01430.1; -.
DR HSSP; P05231; 1IL6.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRINTS; PR00434; INTERLEUKIN_6; 1.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Acute phase; Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 26 By similarity.
FT CHAIN 27 209 Interleukin-6.
FT DISULFID 69 75 By similarity.
FT DISULFID 98 108 By similarity.
SQ SEQUENCE 209 AA; 23483 MW; 75144922B43B48E9 CRC64;
Query Match 52.4%; Score 54; DB 1; Length 209;
Best Local Similarity 42.1%; Pred.No. 2.6;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKKLADGFFFE 19
DB 102 GFNETCLTRITTTGLLEFQ 120
||||: |||: |||:
102 GFNETCLTRITTTGLLEFQ 120

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Job time : 20.9372 secs